

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:07:41 ; Search time 41.5664 Seconds
(without alignments)
2041.789 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKRLCLLYALNLL.....IFETSMTANSFNTHPEMSEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/2/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubaa/US09_PUBCOMB.pep.*
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11: /cgn2_6/prodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubaa/US10A_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubaa/US160_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642	100.0	305	10	US-09-946-374-273
2	1642	100.0	305	12	US-10-176-483-324
3	1642	100.0	305	12	US-10-176-483-324
4	1642	100.0	305	12	US-10-176-483-324
5	1642	100.0	305	12	US-10-176-483-324
6	1642	100.0	305	12	US-10-176-483-324
7	1642	100.0	305	12	US-10-176-483-324
8	1642	100.0	305	12	US-10-176-483-324
9	1642	100.0	305	12	US-10-176-483-324
10	1642	100.0	305	12	US-10-176-483-324
11	1642	100.0	305	12	US-10-176-483-324
12	1642	100.0	305	12	US-10-176-483-324
13	1642	100.0	305	12	US-10-176-483-324
14	1642	100.0	305	12	US-10-176-483-324
15	1642	100.0	305	12	US-10-176-483-324

ALIGNMENTS

RESULT 1

US-09-946-374-273
Sequence 273, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

154, 83,84

[illegible]

; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1642; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVVEAVILTYF 60
QY 61 PVHPVMIACCFLIIVGMLGCGTVKRNLLLLAWYFGLSLVIFCVELACGVTYEQELM 120
DB 61 PVHPVMIACCFLIIVGMLGCGTVKRNLLLLAWYFGLSLVIFCVELACGVTYEQELM 120
QY 121 VPVQSDMVTLKARNTNYGLPRYRWLTHAWNFFQREKCGVYFTDWMLEMDWPPDS 180
DB 121 VPVQSDMVTLKARNTNYGLPRYRWLTHAWNFFQREKCGVYFTDWMLEMDWPPDS 180
QY 181 CVREPPGCSQAHOEDLSLYQEGCGKMYSLRGTKQLQVRLFLGIGISGVTQILAMIL 240
DB 181 CVREPPGCSQAHOEDLSLYQEGCGKMYSLRGTKQLQVRLFLGIGISGVTQILAMIL 240
QY 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
DB 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
QY 301 EMEEL 305
DB 301 EMEEL 305

RESULT 2
US-10-206-915-324
; Sequence 324, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVVEAVILTYF 60
QY 61 PVHPVMIACCFLIIVGMLGCGTVKRNLLLLAWYFGLSLVIFCVELACGVTYEQELM 120
DB 61 PVHPVMIACCFLIIVGMLGCGTVKRNLLLLAWYFGLSLVIFCVELACGVTYEQELM 120
QY 121 VPVQSDMVTLKARNTNYGLPRYRWLTHAWNFFQREKCGVYFTDWMLEMDWPPDS 180
DB 121 VPVQSDMVTLKARNTNYGLPRYRWLTHAWNFFQREKCGVYFTDWMLEMDWPPDS 180
QY 181 CVREPPGCSQAHOEDLSLYQEGCGKMYSLRGTKQLQVRLFLGIGISGVTQILAMIL 240
DB 181 CVREPPGCSQAHOEDLSLYQEGCGKMYSLRGTKQLQVRLFLGIGISGVTQILAMIL 240
QY 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
DB 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
QY 301 EMEEL 305
DB 301 EMEEL 305

RESULT 3
US-10-199-670-324¹
; Sequence 324, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430PLC464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 324
LENGTH: 305
TYPE: PRT
ORGANISM: Homo Sapien
US-10-199-670-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWMDYLNNVLTTLTAETREVEAVILTYF	60
Db	1	MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWMDYLNNVLTTLTAETREVEAVILTYF	60
Qy	61	PVHPVMIACVCCFLIIIVGMLGYCGTVKRNLLLLAWYFSGLLVFCVELACGVWVYQELM	120
Db	61	PVHPVMIACVCCFLIIIVGMLGYCGTVKRNLLLLAWYFSGLLVFCVELACGVWVYQELM	120
Qy	121	VPVQSDMTLTKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWMLEMDWPPDS	180
Db	121	VPVQSDMTLTKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWMLEMDWPPDS	180
Qy	181	CCVREFPGCSKQAHQEDLSLYOEGGCKMYSLRGTKQLQVLRFLGISIGVTOILAMIL	240
Db	181	CCVREFPGCSKQAHQEDLSLYOEGGCKMYSLRGTKQLQVLRFLGISIGVTOILAMIL	240
Qy	241	TITLLWALYYDRREPQTDQWMSLKNDSOHLSCPSVELLKPSLSRIFFTSMNSFNTHF	300
Db	241	TITLLWALYYDRREPQTDQWMSLKNDSOHLSCPSVELLKPSLSRIFFTSMNSFNTHF	300
Qy	301	EMEEL 305	
Db	301	EMEEL 305	

RESULT 4
US-10-201-858-324
Sequence 324, Application US/10201858
Publication No. US2004003837A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430PLC464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 324
LENGTH: 305
TYPE: PRT
ORGANISM: Homo Sapien
US-10-201-858-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWMDYLNNVLTTLTAETREVEAVILTYF	60
Db	1	MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWMDYLNNVLTTLTAETREVEAVILTYF	60
Qy	61	PVHPVMIACVCCFLIIIVGMLGYCGTVKRNLLLLAWYFSGLLVFCVELACGVWVYQELM	120
Db	61	PVHPVMIACVCCFLIIIVGMLGYCGTVKRNLLLLAWYFSGLLVFCVELACGVWVYQELM	120
Qy	121	VPVQSDMTLTKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWMLEMDWPPDS	180
Db	121	VPVQSDMTLTKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWMLEMDWPPDS	180
Qy	181	CCVREFPGCSKQAHQEDLSLYOEGGCKMYSLRGTKQLQVLRFLGISIGVTOILAMIL	240
Db	181	CCVREFPGCSKQAHQEDLSLYOEGGCKMYSLRGTKQLQVLRFLGISIGVTOILAMIL	240
Qy	241	TITLLWALYYDRREPQTDQWMSLKNDSOHLSCPSVELLKPSLSRIFFTSMNSFNTHF	300
Db	241	TITLLWALYYDRREPQTDQWMSLKNDSOHLSCPSVELLKPSLSRIFFTSMNSFNTHF	300
Qy	301	EMEEL 305	
Db	301	EMEEL 305	

RESULT 5
US-10-205-890-324
Sequence 324, Application US/10205890
Publication No. US20040048334A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

APPLICANT: Gurney,Austin L.
APPLICANT: Pan,James
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C519
CURRENT APPLICATION NUMBER: US/10/205,890
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 324
LENGTH: 305
TYPE: PRT
ORGANISM: Homo Sapien
US-10-205-890-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVEEAVILTYF 60
Db 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVEEAVILTYF 60
QY 61 PVVHPVMIAYCCFLIIIVGMLGYCGTVKRNLLLLAWYFGSLIVFCVELACGVWTYEQELM 120
Db 61 PVVHPVMIAYCCFLIIIVGMLGYCGTVKRNLLLLAWYFGSLIVFCVELACGVWTYEQELM 120
QY 121 VPVQWSDMTLKAEMTYGLPRYRLTHAWNFFQREPKCCGVYFTDWMETMDWPPDS 180
Db 121 VPVQWSDMTLKAEMTYGLPRYRLTHAWNFFQREPKCCGVYFTDWMETMDWPPDS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGIGVTOILAMIL 240
Db 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGIGVTOILAMIL 240
QY 241 TITLLWALYDRREPFGTDQWMSLKNDSOHLSCPSVELLKPSLSRIPEHTSMANSFNTHF 300
Db 241 TITLLWALYDRREPFGTDQWMSLKNDSOHLSCPSVELLKPSLSRIPEHTSMANSFNTHF 300
QY 301 EMEEL 305
Db 301 EMEEL 305
RESULT 6
US-10-208-024-324
Sequence 324, Application US/10208024
Publication No. US20040048335A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C538
CURRENT APPLICATION NUMBER: US/10/208,024
CURRENT FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 324
LENGTH: 305
TYPE: PRT
ORGANISM: Homo Sapien
US-10-208-024-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVEEAVILTYF 60
Db 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVEEAVILTYF 60
QY 61 PVVHPVMIAYCCFLIIIVGMLGYCGTVKRNLLLLAWYFGSLIVFCVELACGVWTYEQELM 120
Db 61 PVVHPVMIAYCCFLIIIVGMLGYCGTVKRNLLLLAWYFGSLIVFCVELACGVWTYEQELM 120
QY 121 VPVQWSDMTLKAEMTYGLPRYRLTHAWNFFQREPKCCGVYFTDWMETMDWPPDS 180
Db 121 VPVQWSDMTLKAEMTYGLPRYRLTHAWNFFQREPKCCGVYFTDWMETMDWPPDS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGIGVTOILAMIL 240
Db 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGIGVTOILAMIL 240
QY 241 TITLLWALYDRREPFGTDQWMSLKNDSOHLSCPSVELLKPSLSRIPEHTSMANSFNTHF 300
Db 241 TITLLWALYDRREPFGTDQWMSLKNDSOHLSCPSVELLKPSLSRIPEHTSMANSFNTHF 300
QY 301 EMEEL 305
Db 301 EMEEL 305

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RESULT 7
US-10-201-853-324
; Sequence 324, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-324

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEITRVEAVILTYF 60
Db 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEITRVEAVILTYF 60
QY 61 PVVHPVMIACCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVTYEQELM 120
Db 61 PVVHPVMIACCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVTYEQELM 120
QY 121 VPVQWSDMTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDLEMTDMPDPS 180
Db 121 VPVQWSDMTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDLEMTDMPDPS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMIL 240
Db 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMIL 240
QY 241 TITLLWALYDRRPGTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
Db 241 TITLLWALYDRRPGTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
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RESULT 8
US-10-063-745-108
; Sequence 108, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-108

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEITRVEAVILTYF 60
Db 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEITRVEAVILTYF 60
QY 61 PVVHPVMIACCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVTYEQELM 120
Db 61 PVVHPVMIACCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVTYEQELM 120
QY 121 VPVQWSDMTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDLEMTDMPDPS 180
Db 121 VPVQWSDMTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDLEMTDMPDPS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMIL 240
Db 181 CCVREFPGCSKQAHQEDLSLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMIL 240
QY 241 TITLLWALYDRRPGTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
Db 241 TITLLWALYDRRPGTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

QY 301 EMEEL 305
Db 301 EMEEL 305

RESULT 9
US-10-063-512-108
; Sequence 108, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
```

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-108

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
QY 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
DB 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
QY 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
DB 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
DB 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
QY 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFHTSMANSFNTHF 300
DB 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFHTSMANSFNTHF 300
QY 301 EMEEL 305
DB 301 EMEEL 305

RESULT 10
US-10-063-513-108
; Sequence 108, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-108

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;

Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
QY 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
DB 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
QY 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
DB 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
DB 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
QY 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFHTSMANSFNTHF 300
DB 241 TITLLWALYDRREPFGTDQMSLNKDNSQHLSCPSVELLKPSLSRIFHTSMANSFNTHF 300
QY 301 EMEEL 305
DB 301 EMEEL 305

RESULT 11
US-10-063-515-108
; Sequence 108, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-108

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNNVLTTLTAETRVVEAVILTYF 60
QY 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
DB 61 PVVHPVMIACVCCFLIIIVGMLGCGTKVKNLLLLAWFGSLVIFCVELACGWTYEQELM 120
QY 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
DB 121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDWPPDS 180
QY 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
DB 181 CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240


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; ORGANISM: Homo Sapien
; US-10-063-551-108
Query Match      100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MARESVKLCRLCLLALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVEEAVILTYF 60
DB      1  MARESVKLCRLCLLALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVEEAVILTYF 60

QY      61  PVVHPVMIACVCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLIIVFCVELACGWTYEQELM 120
DB      61  PVVHPVMIACVCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLIIVFCVELACGWTYEQELM 120

QY      121  VPQNSDMWTLKARMTNYGLPSYRMLTHAWNFFQREKCCGVVYFTDMLXEMTMDWPPDS 180
DB      121  VPQNSDMWTLKARMTNYGLPSYRMLTHAWNFFQREKCCGVVYFTDMLXEMTMDWPPDS 180

QY      181  CCVREPPGSKQAHQEDLSLYQEGCGKMYSFRLGTQKQLVRLFLGISIGVTQILAMIL 240
DB      181  CCVREPPGSKQAHQEDLSLYQEGCGKMYSFRLGTQKQLVRLFLGISIGVTQILAMIL 240

QY      241  TITLLWALYDRREPCTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
DB      241  TITLLWALYDRREPCTDQMSLKNDSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

QY      301  ENEEL 305
DB      301  ENEEL 305

RESULT 15
US-10-174-581-324
; Sequence 324, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-26
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
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; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
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; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
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;; PRIOR FILING DATE: 1998-06-12
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;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVEEAVILTYF	60
Db	1	MAREDSVKLCRLCLLYALNLLFWLMSISVLAVSAMRDYLNNVLTTLTAETRVEEAVILTYF	60
Qy	61	PVHPVMIACCFLIIIVGMLGYCGTGVKRNLLLLAWYFGSLLVIFCVELACGWWTYQELM	120
Db	61	PVHPVMIACCFLIIIVGMLGYCGTGVKRNLLLLAWYFGSLLVIFCVELACGWWTYQELM	120
Qy	121	VPVOWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMTDWPDDS	180
Db	121	VPVOWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMTDWPDDS	180
Qy	181	CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSELRGTQQLQVLRFLGISIGVTQILAMIL	240
Db	181	CCVREFPGCSKQAHQEDLSLYQEGCGKKMYSELRGTQQLQVLRFLGISIGVTQILAMIL	240
Qy	241	TITLLWALYYDRREPQDQMSLKNDNSOHLSCPSVELLKPSLSRIFEHTSMANSFNTHF	300
Db	241	TITLLWALYYDRREPQDQMSLKNDNSOHLSCPSVELLKPSLSRIFEHTSMANSFNTHF	300
Qy	301	EMEEL 305	
Db	301	EMEEL 305	

Search completed: May 13, 2004, 16:17:16
Job time : 43.5664 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:00:55 ; Search time 11.3363 Seconds
(without alignments)
1400.935 Million cell updates/sec

Title: US-09-830-328C-2

Perfect score: 1642
Sequence: 1 MAREDSVKCLRLYALNLL.....IPEHTSMANSFNTHFEMBEL 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642	100.0	305	1 T412 HUMAN	O95859 homo sapien
2	292	17.8	253	1 C151 RAT	O93466 rattus norv
3	284	17.3	253	1 C151 MOUSE	O35566 mus musculu
4	279	17.0	239	1 TNES HUMAN	O75594 homo sapien
5	272	16.6	253	1 C151 HUMAN	O48509 homo sapien
6	269	16.4	253	1 C151_CERAE	O95857 cercopithec
7	264	16.1	238	1 T4S7 MOUSE	O9dck3 mus musculu
8	259	15.8	238	1 T4S7 HUMAN	O14817 homo sapien
9	255.5	15.6	237	1 CD63 HUMAN	O28709 oryctolagus
10	250.5	15.3	237	1 CD63 HUMAN	P08962 homo sapien
11	244	14.9	226	1 CD63_BOVIN	O9xak2 bos taurus
12	237.5	14.5	237	1 CD63_RAT	P28648 rattus norv
13	237.5	14.5	267	1 CD82 HUMAN	P27701 homo sapien
14	227.5	13.9	237	1 CD63 MOUSE	P41731 mus musculu
15	220.5	13.4	225	1 CD9_FIG	O8wmq3 sus scrofa
16	214.5	13.1	227	1 CD9_HUMAN	P21926 homo sapien
17	213.5	13.0	225	1 CD9_BOVIN	P30932 bos taurus
18	213.5	13.0	225	1 CD9_FELCA	P40239 felis silve
19	212.5	12.9	225	1 CD9_MOUSE	P40240 mus musculu
20	212.5	12.9	227	1 CD9_CERAE	P30409 cercopithec
21	211.5	12.9	225	1 CD9_RAT	P40241 rattus norv
22	210.5	12.8	221	1 TSN2 RAT	O9j1w1 rattus norv
23	209.5	12.8	217	1 TSN2 MOUSE	O92216 mus musculu
24	204	12.4	237	1 T4S3 HUMAN	P19075 homo sapien
25	201	12.2	236	1 CD81_SAGOE	O9n0j9 saginus oe
26	199	12.1	236	1 CD81_HUMAN	P60033 homo sapien
27	199	12.1	236	1 CD81_PANTR	P60034 pan troglod
28	199	12.1	236	1 CD81 RAT	O62745 rattus norv
29	193.5	11.8	218	1 CD53 MOUSE	O61451 mus musculu
30	193	11.8	236	1 CD81 MOUSE	P35762 mus musculu
31	192.5	11.7	281	1 CD37_HUMAN	P11049 homo sapien
32	191	11.6	249	1 T4S2_HUMAN	P41732 homo sapien
33	190.5	11.6	221	1 TSN2_HUMAN	O60836 homo sapien

34	189	11.5	236	1 CD81_CERAE	O97703 cercopithec
35	189	11.5	249	1 T4S2 MOUSE	O62283 mus musculu
36	189	11.5	253	1 T4S8 MOUSE	O9gy33 mus musculu
37	187	11.4	245	1 T4S6_HUMAN	O43657 homo sapien
38	184.5	11.2	218	1 CD53_RAT	P34495 rattus norv
39	184	11.2	253	1 T4S8_HUMAN	O50637 homo sapien
40	178	10.8	245	1 T4S6 MOUSE	O70401 mus musculu
41	176	10.7	204	1 T413_HUMAN	O95857 homo sapien
42	175.5	10.7	281	1 CD37 MOUSE	O61470 mus musculu
43	175	10.7	266	1 CD82 MOUSE	P40237 mus musculu
44	175	10.7	268	1 T4S9_HUMAN	O50628 homo sapien
45	174.5	10.6	219	1 CD53_HUMAN	P19397 homo sapien

ALIGNMENTS

RESULT 1

T412_HUMAN
ID T412_HUMAN STANDARD; PRT; 305 AA.
AC O95859;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transmembrane 4 superfamily member 12 (Tetraspan NET-2).
GN TM4SF12 OR NET2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=10719184;
RX MEDLINE=20185353; PubMed=10719184;
RA Serru V., Dessen P., Bouchelx C., Rubinstein E.;
RT "Sequence and expression of seven new tetraspans.";
RL Biochim. Biophys. Acta 1478:159-163(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SP) family.
CC
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CC
CC -----
CC EMBL; AF124522; AADI7317.1; -
CC Genew; HGNC:21641; TM4SF12.
CC GO; GO:0016021; C: integral to membrane; TAS.
CC GO; GO:0005624; C: membrane fraction; TAS.
CC InterPro; IPR000301; Transmem_4.
CC Pfam; PF00335; transmembrane4; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; FALSE_NEG.
CC Transmembrane.
CC DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 13 33 POTENTIAL.
CC DOMAIN 34 59 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 60 80 POTENTIAL.
CC DOMAIN 81 89 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 90 110 POTENTIAL.
CC DOMAIN 111 224 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 225 245 POTENTIAL.
CC DOMAIN 246 305 CYTOPLASMIC (POTENTIAL).
CC SEQUENCE 305 AA; 35382 MW; 5EF4D5E1371B92DC CRC64;
SQ

Query Match 100.0%; Score 1642; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 9e-134;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAREDSVKCLRLYALNLLPWLMSISVLAVSANMRDYLNNVLTLTATREVEAVILTYF 60
|||||

Db 1 MAREDSVKLCRLLYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYF 60
 QY 61 PVVHPMIAVCCPLIIVGMLGCGTGVKRNLLLLAWYFGSLVIFCVELACGVWTVYQELM 120
 Db 61 PVVHPMIAVCCPLIIVGMLGCGTGVKRNLLLLAWYFGSLVIFCVELACGVWTVYQELM 120
 QY 121 VPVQWSDMTLTKARMTNYGLPRYRWLTHAWNPFQREKCGGVVYFTDWMLEMTDWPDS 180
 Db 121 VPVQWSDMTLTKARMTNYGLPRYRWLTHAWNPFQREKCGGVVYFTDWMLEMTDWPDS 180
 QY 181 CVVREPPGSKQAHQEDLSLYOEGCGKXGYFLRGTKQLQVLRFLGISIGVTOILAMIL 240
 Db 181 CVVREPPGSKQAHQEDLSLYOEGCGKXGYFLRGTKQLQVLRFLGISIGVTOILAMIL 240
 QY 241 TITLLWALYDRREPCTDMSLKNDNSOHLSCPSVELLKPSLSRIFFHTSWMNSFNTHF 300
 Db 241 TITLLWALYDRREPCTDMSLKNDNSOHLSCPSVELLKPSLSRIFFHTSWMNSFNTHF 300
 QY 301 EMEEL 305
 Db 301 EMEEL 305

RESULT 2
 ID CL151_RAT STANDARD; PRT; 253 AA.
 AC O9QZAG;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Platelet endothelial tetraspan antigen 3 (CD151 antigen).
 GN CD151 OR PETA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=21639251; PubMed=11682256;
 RA Hua L.V., Green M., Wong A., Marsh J.J., Li P.P.;
 RT "Tetraspan protein CD151, a common target of mood stabilizing drugs?";
 RL Neuropharmacology 45:729-736(2001).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; AF192547; AAF05763.2; -.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; transmembrane4_1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane; Lipoprotein; Palmitate.
 FT DOMAIN 1 18
 FT TRANSMEM 19 39
 FT DOMAIN 40 57
 FT TRANSMEM 58 78
 FT DOMAIN 79 91
 FT TRANSMEM 92 112
 FT DOMAIN 113 221
 FT TRANSMEM 222 242
 FT DOMAIN 243 253
 FT TRANSMEM 11 11
 FT LIPID 15 15
 FT LIPID 242 242
 FT LIPID 243 243

FT CARBOHYD 159 159 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 253 AA; 28355 MW; 51876AF31B4DCB2B CRC64;
 Query Match 17.8%; Score 292; DB 1; Length 253;
 Best Local Similarity 29.9%; Pred. No. 5.4e-18;
 Matches 76; Conservative 48; Mismatches 96; Indels 34; Gaps 9;
 QY 9 CLRCLLYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYFPVHPVMI 68
 Db 15 CLKYLLFTYKCCFLWAGLAVNAVGIWTLALKSYISLASS-----TYLATAY-ILV 65
 QY 69 AVCCFLIIVGMLGCGTGVKRNLLLLAWYFGSLVIFCVELACGV--WYEQELMWVQWS 126
 Db 66 VAGVWVMTVGLGCCATFKERRNLLRFLYFILLIIFLEIIAGILAYVYVYQQLNTELKEN 125
 QY 127 DMVTLKARMTNYGLPRYRWLTHAWNPFQREKCGGVVYFTDWMLEMTDWM----- 176
 Db 126 LKDTMKRYHQSG---HEGVINAVDKLOQEFHCCGNSNSRDW---RDSEWIRSGEADSRV 179
 QY 177 PPDSCCVREPPGSKQAHQEDLSLY--QEGCGKXGYFLRGTKQLQVLRFLGISIGVTO 234
 Db 180 VPDSCCKTVVTGCKREH---ASNIYKVEGCITKLESFIQ--EHLRVIGAVGIGIACVQ 234
 QY 235 ILAMILITILLWAL 248
 Db 235 VFGMIPTCCLYRSL 248

RESULT 3
 ID CL151_MOUSE STANDARD; PRT; 253 AA.
 AC O35566; O89118;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Platelet-endothelial tetraspan antigen 3 (PETA-3) (GP27) (Membrane
 DE Glycoprotein SFA-1) (CD151 antigen).
 GN CD151 OR PETA3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=97438231; PubMed=9294006;
 RA Hasegawa H., Watanabe H., Nomura T., Utsunomiya Y., Yanagisawa K.,
 RA Fujita S.;
 RT "Molecular cloning and expression of mouse homologue of SFA-1/PETA-3
 RT (CD151), a member of the transmembrane 4 superfamily.";
 RL Biochim. Biophys. Acta 1353:125-130(1997).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=98267146; PubMed=9602068;
 RA Fitter S., Seldin M.F., Ashman L.K.;
 RT "Characterisation of the mouse homologue of CD151 (PETA-3/SFA-1);
 RT genomic structure, chromosomal localisation and identification of 2
 RT novel splice forms.";
 RL Biochim. Biophys. Acta 1398:75-85(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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 DR EMBL; D89290; BAA22447.1; -.
 DR EMBL; AF033820; AAC25952.1; -.
 DR EMBL; U09772; AAC25976.1; -.


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CC EMBL; AF089749; AAC35859.1; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005824; C:membrane fraction; TAS.
CC InterPro; IPR000301; Transmem_4.
CC Pfam; PF00335; transmembrane4; 1.
CC PRINTS; PR00259; TMPOUR.
CC PROSITE; PS00421; TW4.1; 1.
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 14 34 POTENTIAL..
FT DOMAIN 35 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 76 POTENTIAL.
FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 224 POTENTIAL..
FT DOMAIN 225 239 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL) .
SQ SEQUENCE 239 AA; 26779 MW; DD7BA332BF6584EB CRC64;
Query Match 17.0%; Score 279; DB 1; Length 239;
Best Local Similarity 28.9%; Pred No. 6.6e-17;
Matches 74; Conservative 41; Mismatches 103; Indels 38; Gaps 7;
QY 9 CLRCLLXALNLLFLWMSISVLVSAWRDYLNNVLTALTATREVBAAVILTVFVVHP--V 66
DB 8 CLKYMFMLFNLIPLFCGCLLGIVGLWSQGNAFTSPS-----FPSLSAANL 56
QY 67 MIAVCCFLIIIVGLGYCGTKVKNLILLAWFGSLIIVFCVELACGWITVEQLMYPVQWS 126
DB 57 VLAIGTIVVGFVGCGIGALKENKULLGFFVILLVILLAEIL-----LIDFFVM 108
QY 127 DMVT-----LKARMTNYGLPRYLWLTHAWNFFQREFKCGGVYFTDWMLEMDWPDPDS 180
DB 109 DKVWENAKDLKEGLLYHTENNVLKNWNIIQAEMRCCGVTDVDWYPVLGENTVPDR 168
QY 181 CVREFPGCSKQAHQEDLDLDLYEGCGKKMYSFRLGTRKOLQVLRPLGISIGVTILAMIL 240
DB 169 CMENSQCGRNA---TFPLWRTGCYEKWKVWFDDNK--HVLGTGVGMCIIMQLGNAF 222
QY 241 TITTLWALY-----YD 251
DB 223 SMTLFQHHRFGKYD 238
RESULT 5
C151 HUMAN
ID C151 HUMAN STANDARD; PRT; 253 AA.
AC P48509; O14826; Q96TE3;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Platelet-endothelial tetraspan antigen 3 (PETA-3) (GP27) (Membrane glycoprotein SFA-1) (CD151 antigen).
GN GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RR TISSUE=Platelet;
RX MEDLINE=95359431; PubMed=7632941;
RA Fitter S., Tetaz T.J., Berndt M.C., Ashman L.K.;
RT "Molecular cloning of cDNA encoding a novel platelet-endothelial cell tetra-span antigen, PETA-3."
RL Blood 86:1348-1355(1995).
RN [2]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=96186759; PubMed=8627808;
 RA Hasegawa H., Utsunomiya Y., Kishimoto K., Yanagisawa K., Fujita S.;
 RT "SFA-1, a novel cellular gene induced by human T-cell leukemia virus
 type 1, is a member of the transmembrane 4 superfamily.";
 RL J. Virol. 70:3258-3263(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=1181065;
 RA Whitlock N.V., McLean W.H.I.;
 RT "Genomic organization, amplification, fine mapping, and intragenic
 RT polymorphisms of the human hemidesmosomal tetraspanin CD151 gene.";
 RL Biochem. Biophys. Res. Commun. 281:425-430(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, and Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerbber B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PALMITOYLATION.
 RX MEDLINE=21904786; PubMed=11907260;
 RA Yang X., Claas C., Kraeft S.K., Chen L.B., Wang Z., Kreidberg J.A.,
 RA Hemler M.E.;
 RT "Palmitoylation of tetraspanin proteins: modulation of CD151 lateral
 RT interactions, subcellular distribution, and integrin-dependent cell
 RT morphology.";
 RL Mol. Biol. Cell 13:767-781(2002).
 CC -1- SUBUNIT: Interacts with integrins alpha3beta1, alpha3beta2,
 CC alpha3beta4 and alpha6beta4, with CD9 and CD181.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues including
 CC vascular endothelium and epidermis.
 CC -1- INDUCTION: BY HTLV-1.
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -1- DATABASE: NAMP=PROW; NOTE=CD guide CD151 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd151.htm".
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 CC EMBL; D29963; BAA06229.1; -;
 CC EMBL; AF315942; AAK14179.1; -;
 CC EMBL; BC001374; AAK01374.1; -;
 CC EMBL; BC013302; AAK13302.1; -;
 CC EMBL; HGNC:1630; CD151.
 CC MIM; 602243; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005624; C:membrane fraction; TAS.

DR InterPro: IPR000301; Transmem 4.
 DR Pfam: PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane; Polymorphism; Lipoprotein; Palmitate.
 FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 19 39 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 40 57 POTENTIAL.
 FT TRANSMEM 58 78 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 79 91 POTENTIAL.
 FT TRANSMEM 92 112 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 113 221 POTENTIAL.
 FT TRANSMEM 222 242 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 243 253 S-palmitoyl cysteine.
 FT LIPID 11 15 S-palmitoyl cysteine.
 FT LIPID 15 15 S-palmitoyl cysteine.
 FT LIPID 242 242 S-palmitoyl cysteine.
 FT LIPID 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 159 159 R -> K.
 FT VARIANT 132 132 /FTID=VAR_012490.
 FT VARIANT 137 137 S -> P.
 FT VARIANT 137 137 /FTID=VAR_012491.
 SQ SEQUENCE 253 AA; 28313 MW; 5C81D7D62D750EAF CRC64;
 Query Match 16.6%; Score 272; DB 1; Length 253;
 Best Local Similarity 29.4%; Pred. No. 2.8e-16;
 Matches 75; Conservative 46; Mismatches 98; Indels 36; Gaps 10;
 Qy 9 CLRCILYALNLLFLWMSISVLAVSAMRDYLNVLTLTAETRVAAVILTPVPHVPMI 68
 Db 15 CLKYLLFTYNCCEFWAGLAWAVGIVTLAKSDYISLLASG-----TYLATAY-ILV 65
 Qy 69 AVCCFLIIIVGMLGCGTFRKRNLLLLWYFGLSLAVIFCVELACGV--WTYEQLMVPVQWS 126
 Db 66 VAGTVVWVTVGLCCGATFKERNLLRLLYFILLIIFLLBIAGILAYAYVQNLTELK-- 123
 Qy 127 DMVTLKARMT-NYGLPRYRLWTHANFFQRFKCCGVVYFTDLEMTEDM----- 176
 Db 124 --ENLKDVTTRYHQSHEAVTSVDOLOQEFHCCGNSNSQDM---RDSEWIRSQEAGGR 178
 Qy 177 -PDSCCVRFPFGCKQKQHQEDLSLY--QEGCKKMYSFRLGKQLQVLRFLGIGT 233
 Db 179 VPDSCCKTVVLCGQGDH---ASNIYKVEGGITKLETFIQ--EHLRVIGAVGIGIACV 233
 Qy 234 QILAMILTITLLMAL 248
 Db 234 QVFGMIPTCCLYRSL 248
 RESULT 6
 CL151_CERAE STANDARD; PRT; 253 AA.
 ID CL151_CERAE
 AC QNMYM2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Platelet-endothelial tetraspan antigen 3 (PETA-3) (CD151 antigen).
 GN CD151.
 OS Cercopithecus aethiops (Green monkey) (Grivet), and
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534, 9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shanmukhappa K., Kapil S.;
 RT "CD151/PETA-3, a tetraspanin molecule, interacts with the 3'
 RT untranslated region and partial nucleoprotein gene of porcine
 RT reproductively and respiratory syndrome virus RNA.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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 CC EMBL; AF275665; RAF90151.1; --
 CC EMBL; AF275666; RAF90152.1; --
 CC InterPro: IPR000301; Transmem_4
 CC Pfam; PF00335; Transmembrane4; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4_1; 1.
 CC Glycoprotein; Transmembrane; Lipoprotein; Palmitate.
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 1 18
 CC TRANSMEM 19 39
 CC DOMAIN 40 57
 CC TRANSMEM 58 78
 CC DOMAIN 79 91
 CC TRANSMEM 92 112
 CC DOMAIN 113 221
 CC TRANSMEM 222 242
 CC DOMAIN 243 253
 CC TRANSMEM 253 269
 CC LIPID 11 11
 CC LIPID 15 15
 CC LIPID 242 242
 CC LIPID 243 243
 CC CARBOHYD 159 159
 CC SEQUENCE 253 AA; 28438 MW; CAD2780B63F644A CRC64;
 Query Match 16.4%; Score 269; DB 1; Length 253;
 Best Local Similarity 28.6%; Pred. No. 5.1e-16;
 Matches 72; Conservative 48; Mismatches 102; Indels 30; Gaps 8;
 QY 9 CLRLCYALNLFWMISVLAVSAMRDYLNVLTLTAETRVBAVILTPVPVHPVMI 68
 Db 15 CLKYLLFTYVNCFFWLAGLAVMVGWTLAKSDYISLLASG-----TYLATAY-ILV 65
 QY 69 AVCCFLIIVGMGYCGTVKRNLLLAIFPGSLIVFCVELAGCV--WTYBELMVPVMS 126
 Db 66 VAGAVVMVTGVLGCCATKPERENLRPLFILLIIFLLEITAGVLAVYVYQQLNTELKEN 125
 QY 127 DMVTLKARTNYGLPRYRLTHAWNFFQREKPCGCVVYFTDMLWEMTDW----- 176
 Db 126 LKDTWAKR--YHQPGHEAVTSVQLQOEFFCCSNNSDW---RDSWRLRARGRV 179
 QY 177 PPSDCVREFPCCSKQAQEDLSDLYQSCGCKMYSFLRGTKQLQVRLFGISGVQIL 236
 Db 180 VPDSCCKTVAGCGQDRHAFNIYKV-EGGFITKLETFQ--EHLRVIGAVGTGIACVQVF 236
 QY 237 AMILITILLWAL 248
 Db 237 GMIFTCCLYRSL 248
 RESULT 7
 T4S7 MOUSE STANDARD; PRT; 238 AA.
 ID T4S7 MOUSE
 AC Q9DCK3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Transmembrane 4 superfamily, member 7.
 GN TM4SF7.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Szaubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBUNIT: FORMS A COMPLEX WITH INTEGRINS (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -----
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 CC -----
 CC EMBL; AK002709; BAB22301.1; --
 CC EMBL; BC003482; AAH03482.1; --
 CC MGD; MGI:1928097; Tm4sf7.
 CC InterPro: IPR000301; Transmem_4
 CC Pfam; PF00335; Transmembrane4; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4_1; 1.
 CC Glycoprotein; Transmembrane.
 CC DOMAIN 1 13
 CC TRANSMEM 14 34
 CC POTENTIAL.
 CC DOMAIN 35 55
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 56 76
 CC POTENTIAL.
 CC DOMAIN 77 85
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 86 106
 CC POTENTIAL.
 CC DOMAIN 107 201
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 202 222
 CC POTENTIAL.

FT DOMAIN 223 238 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 238 AA; 26053 MW; AA916BF6078777FA CRC64;
 Query Match 16.1%; Score 264; DB 1; Length 238;
 Best Local Similarity 28.3%; Pred. No. 1.3e-15;
 Matches 73; Conservative 46; Mismatches 93; Indels 46; Gaps 9;
 QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYF 60
 DB 1 MAR-CGLQKYLMEAFNLLFWLGGCGVLGGVGLGIMLAATQGNFATLSSS-----F 48
 QY 61 PVVHP--VMIAVCCFLIIIVGMLGYCGTVKRNLLLLAWFGSLIVFCVELACGWTYQOE 118
 DB 49 PLSAANLLIITGTFVMAIGFVCCGALKENKCLLTFFVLLLVFLLEATIAIFF--- 105
 QY 119 LMPVQWSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQRFKCGGVYFTDWMLEMT 172
 DB 106 -----AYSDKIDSYAQDLKKGHLHYGTQGNVGLTNAMSIIQTDFRCGCGVNYTDWEVY 160
 QY 173 EMDWPPDSCVREFFPGCSKQAOHQEDLSLYQEGCGKMYSFRLGKQLQVFLGISIGV 232
 DB 161 NATRVPDSCCL-EP-----SDSCGLHEPGTWMKSPCYETVKAWLQ--ENLLAVGIF 208
 QY 227 GISIGVTOILAMILITL 244
 DB 209 GLCTALVQILGTFAMTM 226
 RESULT 8
 ID T4S7 HUMAN STANDARD; PRT; 238 AA.
 AC 014817;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Transmembrane 4 superfamily, member 7 (Novel antigen 2) (NAG-2)
 DE (Tetraspanin 4) (Tspan-4).
 GN T4S7F7 OR NAG2 OR TSPAN4.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98030601; PubMed=9360996;
 RA Tachibana I., Bodorova J., Berdichevski F., Zutter M.M., Hemler M.E.,
 RT "NAG-2, a novel transmembrane 4 superfamily (T4S7F) protein that
 RL complexes with integrins and other T4S7F proteins.";
 RL J. Biol. Chem. 272:29181-29189(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98390278; PubMed=9714763;
 RA Todd S.C., Doctor V.S., Levy S.;
 RT "Sequences and expression of six new members of the tetraspanin/T4S7
 RL family.";
 RL Biochim. Biophys. Acta 1399:101-104(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBUNIT: FORMS A COMPLEX WITH INTEGRINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MULTIPLE TISSUES BUT IS ABSENT IN
 CC BRAIN, LYMPHOID CELLS, AND PLATELETS.
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF022813; AAC51864.1; -;
 CC EMBL; AF054841; AAC69717.1; -;
 CC EMBL; BC000389; AAH00389.1; -;
 CC EMBL; BC019314; AAH19314.1; -;
 CC PIR; A59265; A59265;
 CC Genew; HGNC:11859; TM4SF7.
 CC MIM; 602644; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0006461; P:protein complex assembly; TAS.
 CC InterPro; IPR000301; Transmem 4.
 CC Pfam; PF00335; transmembrane4; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane.
 FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 14 34 POTENTIAL.
 FT DOMAIN 35 55 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 56 76 POTENTIAL.
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 POTENTIAL.
 FT DOMAIN 107 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 222 POTENTIAL.
 FT DOMAIN 223 238 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 238 AA; 26118 MW; A6B9A5633065A492 CRC64;
 Query Match 15.8%; Score 259; DB 1; Length 238;
 Best Local Similarity 27.0%; Pred. No. 3.4e-15;
 Matches 68; Conservative 48; Mismatches 102; Indels 34; Gaps 7;
 QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYF 60
 DB 1 MAR-CGLQKYLMEAFNLLFWLGGCGVLGGVGLGIMLAATQGNFATLSSS-----AATQGSFATLSSSF 48
 QY 61 PVVHP--VMIAVCCFLIIIVGMLGYCGTVKRNLLLLAWFGSLIVFCVELACGWTYQOE 118
 DB 49 PLSAANLLIITGTFVMAIGFVCCGALKENKCLLTFFVLLLVFLLEATIAIFF--- 105
 QY 119 LMPVQWSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQRFKCGGVYFTDWMLEMT 172
 DB 106 -----AYTKIDRYAQDLKKGHLHYGTQGNVGLTNAMSIIQTDFRCGCGVNYTDWEVY 160
 QY 173 EMDWPPDSCVREFFPGCSKQAOHQEDLSLYQEGCGKMYSFRLGKQLQVFLGISIGV 232
 DB 161 NATRVPDSCCLFSESCGLHAP-----GTWKPAPCYETVKAWLQ--ENLLAVGIFGLCTAL 214
 QY 233 TQILAMILITL 244
 DB 215 VQILGTFAMTM 226

180 SCCVREPPGSKQAQEDLSLYOEGCGKMYSLFRTGKOLQVLRFLGIGVTOILAMI 239
 167 SCCVNTSGCGVKF--NVKDIYVEGCVKELGLWLR--KNVLVVAALGIAFVEVLGIV 221

240 ITITLL 245
 222 FACCLV 227

RESULT 10
 CD63 HUMAN
 ID CD63 HUMAN STANDARD; PRT; 237 AA.
 AC P08962;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE CD63 antigen (Melanoma-associated antigen ME491) (Lysosome-associated
 membrane glycoprotein 3) (LAMP-3) (Ocular melanoma-associated
 antigen) (OMA81H) (Granulophysin).
 GN CD63 OR MLAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88210273; PubMed=336586;
 RA Hotta H., Ross A.H., Huebner K., Isobe M., Wendeborn S., Chao M.V.,
 Ricciardi R.P., Tsujimoto Y., Croce C.M., Koprowski H.;
 RT "Molecular cloning and characterization of an antigen associated with
 early stages of melanoma tumor progression.";
 RL Cancer Res. 48:2955-2962(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91131632; PubMed=1993697;
 RA Metzelaar M.J., Wigngaard P.L., Peters P.J., Sixma J.J.,
 Nieuwenhuis H.K., Clevers H.C.;
 RT "CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a
 screening procedure for intracellular antigens in eukaryotic cells.";
 RL J. Biol. Chem. 266:3239-3245(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=91025550; PubMed=2171551;
 RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
 Scheit K.H.;
 RT "Characterization of three abundant mRNAs from human ovarian
 granulosa cells.";
 RL DNA Cell Biol. 9:479-485(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92287132; PubMed=1599482;
 RA Hotta H., Miyamoto H., Hara I., Takahashi N., Homma M.;
 RT "Genomic structure of the ME491/CD63 antigen gene and functional
 analysis of the 5'-flanking regulatory sequences.";
 RL Biochem. Biophys. Res. Commun. 185:436-442(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92181348; PubMed=1339263;
 RA Wang M.X., Earley J.J. Jr., Shields J.A., Donoso L.A.;
 RT "An ocular melanoma-associated antigen. Molecular characterization.";
 RL Arch. Ophthalmol. 110:399-404(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

180 SCCVREPPGSKQAQEDLSLYOEGCGKMYSLFRTGKOLQVLRFLGIGVTOILAMI 239
 167 SCCVNTSGCGVKF--NVKDIYVEGCVKELGLWLR--KNVLVVAALGIAFVEVLGIV 221

240 ITITLL 245
 222 FACCLV 227

RESULT 9
 CD63 RABBIT
 ID CD63 RABBIT STANDARD; PRT; 237 AA.
 AC Q28709;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CD63 antigen.
 GN CD63.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95120837; PubMed=7820873;
 RA Schma Y., Suzuki T., Sasano H., Nagura H., Nose M., Yamamoto T.;
 RT "Increased mRNA for CD63 antigen in atherosclerotic lesions of
 Watanabe heritable hyperlipidemic rabbits.";
 RL Cell Struct. Funct. 19:219-225(1994).
 CC -!- FUNCTION: May play some role in signal transduction pathways.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
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 CC
 CC ENBL; D21264; BAA04804.1; --
 DR PIR; JC2297; JC2297.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4.1; 1.
 KW Glycoprotein; Antigen; Transmembrane; Lysosome.
 FT INITMET 0
 FT DOMAIN 1 10
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31
 FT POTENTIAL.
 FT DOMAIN 32 50
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 51 69
 FT POTENTIAL.
 FT DOMAIN 70 80
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 106
 FT POTENTIAL.
 FT DOMAIN 107 202
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 203 223
 FT POTENTIAL.
 FT DOMAIN 224 237
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 124 124
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 149 149
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171 171
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171 171
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 237 AA; 25498 MW; 063454D727E8A36C CRC64;

Query Match 15.6%; Score 255.5; DB 1; Length 237;
 Best Local Similarity 29.7%; Pred. No. 6.8e-15;
 Matches 73; Conservative 44; Mismatches 108; Indels 21; Gaps 7;

QY 2 ARDSVKLCRLIYALNLLFWLMSISVLAVSAMRWYLNVLTLTAEVVEAVILTYTP 61
 1 AVEGGMKCVFLYLLAFACAVGLIAGVGAQLVLSQTIT-----HGATPGSLLP 53
 62 VHPVMIACVCFILIIIVGLMGYCGTVKRNLLLLAWFGSLIIVPCVLACGVWYEQELMV 121
 54 V---VLIAGAFILYVAFVCGCTCKENYCLMITFAFLSLIMLVEVAAGYVPRDKV 110
 122 PVQSDMVTUKARMTNGLPRYRWLTHANFFOREFKCCGVYFTDNLWEM--DWPPD 179
 111 MSEFNK--DFRQOMNYSTDNTAL--ILDRMQDKFTCCGAANYTDTWIPGTRDRVDP 156

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Valek J.A., Gunaratne P.H., Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalus D.E., Schnzer A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." [7] Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE OF 1-20.
MEDLINE=86049405; PubMed=4062294;
Ross A.H., Diezschold B., Jackson D.M., Earley J.J., Christ B.F.D., Atkinson B., Koprowski H.;
"Isolation and amino terminal sequencing of a novel melanoma-associated antigen." [7] Arch. Biochem. Biophys. 242:540-548(1985).

[8]
CARBOHYDRATE-LINKAGE SITE ASN-129.
MEDLINE=22660472; PubMed=12754519;
Zhang H., Li X.-J., Martin D.B., Aebersold R.;
"Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry." Nat. Biotechnol. 21:660-666(2003).

CC -!- FUNCTION: THIS ANTIGEN IS ASSOCIATED WITH EARLY STAGES OF MELANOMA TUMOR PROGRESSION. MAY PLAY A ROLE IN GROWTH REGULATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC -!- TISSUE SPECIFICITY: DYSPLASTIC NEVI, RADIAL GROWTH PHASE PRIMARY MELANOMAS, HEMATOPOIETIC CELLS, TISSUE MACROPHAGES.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD63 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd63.htm".

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DR EMBL; X07982; CAA30792.1; -;
DR EMBL; M58485; -; NOT ANNOTATED_CDS.
DR EMBL; M59907; AAA63235.1; -;
DR EMBL; X62654; CAA44519.1; -;
DR EMBL; S93788; AAB21617.1; -;
DR EMBL; BC002349; AAB02349.1; -;
DR EMBL; BC013017; AAB13017.1; -;
DR PIR; I38016; I38016.
DR Genew; HGNC:1692; CD63.
DR MIM; 155740; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005765; C:lysosomal membrane; TAS.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR Glycoprotein; Antigen; Transmembrane; Lysosome.
KW INIT MET 0
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 21 POTENTIAL.
FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 69 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 106 POTENTIAL.
FT DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 237 AA; 25505 MW; 0CBG38F931CF0C9B CRC64;
Query Match 15.3%; Score 250.5; DB 1; Length 237;
Best Local Similarity 27.6%; Pred. No. 1.8e-14;
Matches 68; Conservative 52; Mismatches 105; Indels 21; Gaps 7;
QY 2 AREDSVKLCRLIYALNLLFWLMSISVLAVSAMRDYLNWVLTLTAEVVEAVILTFP 61
Db 1 AVEGKMKVFLYLLVLLAFACAVGLIAGV-----GAQLVLSQTIQGFPSLIP 53
QY 62 VHPVMIACVCFLLIIVGMLGYCGTVKRNLLLLAWYFGLSLVIFCVELACGVWYQELMV 121
Db 54 V---VIIAVGVFLVAFVCGCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRKV 110
QY 122 PVQMSDMVTLKARNTNYGLPRYRLTHANFFQREERKCCGVYFTDWLENTM--DWPD 179
Db 111 MSEFNN--NFRQOMENY--PNNHTASILDPMQADFKCGAANYTDWEKIPSKNRVDP 166
QY 180 SCCVREPPFGCSQAHQEDLSLYQEGCGKQVGFRLGTQKQLQVLRFLGISIGVTQILMI 239
Db 167 SCCINVTGCGINFNEK--AIHKEGCVKIGGWLK--KNVLVAAAALGIAFVEVLGIV 221
QY 240 LTTLL 245
Db 222 FACCLV 227
RESULT 11
CD63_BOVIN STANDARD; PRT; 236 AA.
ID CD63_BOVIN STANDARD; PRT; 236 AA.
AC Q9XSK2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CD63 antigen.
GN CD63.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA MEDLINE=99328909; PubMed=10998809;
RX Brooke G.P., Sopp P., Kwong L.S., Howard C.J.;
RT "Molecular cloning of cattle CD63 and evidence for high level expression on subpopulations of dendritic cells." Immunogenetics 49:812-814(1999).
RL Immunogenetics 49:812-814(1999).
CC -!- FUNCTION: May play some role in signal transduction pathways.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal (B; similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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DR EMBL; AJ012589; CAB40564.1; -;
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR Glycoprotein; Antigen; Transmembrane; Lysosome.
KW INIT MET 0
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 60 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 106 POTENTIAL.
FT DOMAIN 107 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 236 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 236 AA; 25648 MW; 91AF09A0B338CE09 CRC64;

Query Match 14.9%; Score 244; DB 1; Length 236;
Best Local Similarity 29.0%; Pred. No. 6.6e-14;
Matches 71; Conservative 46; Mismatches 108; Indels 20; Gaps 7;

QY 2 ARDSVKCLCLYALNLLFLWLSISVLAVSAMWEDYLNVLTLTAETRVVEAVILTYPP 61
DB 1 AVEGKMKCVFLYVLLVFCACAVGLIAGVGVTHLVNQITII-----HGATPSFLIP 53
QY 62 VVHPVMIACVCFLLIIVGMLGCGVTKRNLLLLAWYFGSLVIFCVELACGWTYQELMV 121
DB 54 V--VIIAGAFLLVAFVCGCGACKENYCLMITFAIFLSLIMLVEVAAGVYFRDKV 110
QY 122 PVWSDMTVLKARNTNYGLPRYRWLTHANFFOREFKCCGVYFTDWLENTM--DWPPDS 180
DB 111 RSEFNK--DFRQWKNY--PKDNQTASILDKMQDFECCGAANYTDWEKILVATNKVPDS 166
QY 181 CCVREFPGCKQAHQEDLSLYOEGCGKMYSLRGTKQLQVRLFLGIGISIGVTFQILAMIL 240
DB 167 CCVNIHNCGINF---VVKDIHTEGCVKEKTAWLK--KNVLVVVAAALGIAFVEILGIVL 221
QY 241 TITLL 245
DB 222 ACCIV 226

CC -!- TISSUE SPECIFICITY: ON MAST CELLS & PLATELETS OF RAT TISSUES.
CC INDUCED IN OTHER CELLS IN CULTURE.
CC -!- DEVELOPMENTAL STAGE: INCREASED EXPRESSION OF THE AD1 ANTIGEN IN EMBRYONAL TISSUES.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
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CC
DR EMBL; X61654; CAA43835.1; -.
DR PIR; A46508; A46508.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4.1; 1.
KW Glycoprotein; Antigen; Transmembrane; Lysosome.
FT INIT_MEI 0 0
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 60 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 106 POTENTIAL.
FT DOMAIN 107 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 237 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 237 AA; 25567 MW; 3FE87B6DF3D72854 CRC64;

Query Match 14.5%; Score 237.5; DB 1; Length 237;
Best Local Similarity 28.5%; Pred. No. 2.4e-13;
Matches 72; Conservative 46; Mismatches 100; Indels 35; Gaps 9;

QY 2 ARDSVKCLCLYALNLLFLWLSISVLAVSAMWEDYLNVLTLTAETRVVEAVILTYPP 61
DB 1 AVEGKMKCVFLYVLLVFCACAVGLIAGVGVTHLVNQITII-----HETTAGSLIP 53
QY 62 VVHPVMIACVCFLLIIVGMLGCGVTKRNLLLLAWYFGSLVIFCVELACGWTYQELMV 121
DB 54 V--VIIAGAFLLVAFVCGCGACKENYCLMITFAIFLSLIMLVEVAAGVYFRDQV 110
QY 122 PVWSDMTVLKARNTNYGLPRYRWLTH-----ANFFOREFKCCGVYFTDWLENTM-- 174
DB 111 KSEFSK--SFQKQMONY-----LTDNKTATILDKQENKCCGASNTDWERIPGMAK 161
QY 175 DWPPDSCCVREFPGCKQAHQEDLSLYOEGCGKMYSLRGTKQLQVRLFLGIGISIGV-- 232
DB 162 DRVPDSCCINIVGCGNDFKE---STIHTQCGVETIAAWLR-----KNVLLVAGAAALGIAF 214
QY 233 TQILAMILTITLL 245
DB 215 VEVLGIIIFSCCLV 227

RESULT 12
CD63 RAT STANDARD; PRT; 237 AA.
AC P28648;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE CD63 antigen (AD1 antigen).
GN CD63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=92340890; PubMed=1634775;
RA Nishikata H., Oliver C., Mergenhagen S.E., Siraganian R.P.;
RT "The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen ME491) is expressed in other cells in culture."
RL J. Immunol. 149:862-870(1992).
RN [2]
RP SEQUENCE OF 1-43.
RX MEDLINE=91107696; PubMed=1703158;
RA Kitani S., Berenstein E., Mergenhagen S.E., Tempst P., Siraganian R.P.;
RT "A cell surface glycoprotein of rat basophilic leukemia cells close to the high affinity IgE receptor (Fc epsilon RI). Similarity to human melanoma differentiation antigen ME491."
RJ J. Biol. Chem. 266:1903-1909(1991).
CC -!- FUNCTION: MAY BE INVOLVED IN THE SECRETORY PROCESS OF MAST CELLS AND MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC SECRETORY GRANULES AND PLASMA MEMBRANE OF MANY CULTURED CELL LINES.

RESULT 13
CD82 HUMAN STANDARD; PRT; 267 AA.
ID CD82 HUMAN
AC P27701;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD82 antigen (Inducible membrane protein R2) (C33 antigen) (IA4) (Metastasis suppressor Kangai 1) (Suppressor of tumorigenicity-6).
DE Kaili OR CD82 OR SAR2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NBI_TaxID=9606;

(1)

RN RN

SEQUENCE FROM N.A.

TISSUE=Peripheral blood lymphocytes;

MEDLINE=9115380; Pubmed=1842498;

Gaugitsch H.W., Hofer B., Huber N.E., Schnabl E., Baumruker T.;

"A new superfamily of lymphoid and melanoma cell proteins with extensive homology to Schistosoma mansoni antigen Sm23."; Eur. J. Immunol. 21:377-383(1991).

(2)

RN RN

SEQUENCE FROM N.A.

MEDLINE=93017900; PubMed=1401919;

Inai T., Fukudome K., Takagi S., Nagira M., Furuse M., Fukuhara N., Nishimura M., Hiruma Y., Yoshie O.;

"C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leukemia virus type I-induced syncytium formation is a member of a new family of transmembrane proteins including CD9, CD37, CD53, and CD63"; J. Immunol. 149:2879-2886(1992).

(3)

RN RN

SEQUENCE FROM N.A.

MEDLINE=95273964; PubMed=7754374;

Dong J.T., Barrett J.C.;

"KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p11.2"; Science 268:884-886(1995).

[4]

RN RN

SEQUENCE FROM N.A.

Dong J.;

Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: ASSOCIATES WITH CD4 OR CD8 AND DELIVERS COSTIMULATORY SIGNALS FOR THE TCR/CD3 PATHWAY.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: LYMPHOID SPECIFIC.

-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

-!- DATABASE: NAME=PROW; NOTE=cd guide CD82 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd82.htm".

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EMBL; X53795; CAA37804.1; -
EMBL; S48196; AAB23825.1; -
EMBL; U20770; AAC50133.1; -
EMBL; U67274; AAC51205.1; -
EMBL; U67268; AAC51205.1; JOINED.
EMBL; U67269; AAC51205.1; JOINED.
EMBL; U67270; AAC51205.1; JOINED.
EMBL; U67271; AAC51205.1; JOINED.
EMBL; U67272; AAC51205.1; JOINED.
EMBL; U67273; AAC51205.1; JOINED.
PIR; I38942; A46493.
Genev; HGNC:6210; KAIL.
MIM; 600623; --
GO; GO:0005887; C:integral to plasma membrane; TAS.
InterPro; IPRO00301; Transmem_4.
Pfam; PF00335; Transmembrane4; 1.
PRINTS; PR00259; TMFOUR.
PROSITE; PS00421; TW4.1; 1.
Glycoprotein; Transmembrane; Antigen.
DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
TRANSMEM 12 32 POTENTIAL.
DOMAIN 33 53 EXTRACELLULAR (POTENTIAL).
TRANSMEM 54 72 POTENTIAL.
DOMAIN 73 83 CYTOPLASMIC (POTENTIAL).
TRANSMEM 84 110 POTENTIAL.
DOMAIN 111 228 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	229	250	POTENTIAL.
FT	DOMAIN	251	267	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	240	241	II -> MV (IN REF. 2).
FT	SEQUENCE	267 AA;	29625 MW;	FC379855BBDICABDE CRC64;
Query Match				
Best Local Similarity 27.0%; Pred. No. 2.7e-13;				
Matches 71; Conservative 51; Mismatches 100; Indels 41; Gaps 10;				
QY	7	VKLCRLLYALNLLFWLMSISVLAVAWM----	ROYLNNVLTLTAEATRVEEAVILTYEPPV	62
DB	6	IKVTKYFLFNLFFILGAVILGFGWILADKSPISVLQTSSSLRMG-----	AY---	57
QY	63	VHPVMIACVCCFLIIVGMLGCGYVKKRNLALLAWYFGSLIVFCVELACGVMTYEQELMVP	122	
DB	58	---VFIGVAVTLMGLFCIGAGVNEVRCILGIFYAFLLILLIAQVTAGALFYFNMGKX	114	
QY	123	VQSDMTLTKARNTNYGLPRYRLTHANPFFQREKCCGVYFTDWLEWTE-MKW	177	
DB	115	QEMGGIVTELIR--DYNSSREDSLQADWYVQAQVKCCGWSFYNTWTDNASELMNRPEVTY	172	
QY	178	PDSCCVR-----	REPCCSKQA--HQEDLSLDLYOEGCGKKWYSFLRGTRKQLQ	221
DB	173	PCSEVGEGBEDNLSLVKGFCEAPGNRTQSGNHPEDM-FVYEGCGMCKVQAWLQ--ENLG	229	
QY	222	VLRFGLGISGVTOILAMILITL	244	
DB	230	IILGVGVGVALIELLGNVLSICL	252	
RESULT 14				
ID	CD63 MOUSE	STANDARD;	PRT;	237 AA.
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-NOV-2004 (Rel. 43, Last annotation update)			
DE	CD63 antigen.			
GN	CD63.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=94198294; PubMed=8148377;			
RA	Miyamoto M., Honma M., Hotta H.;			
RT	"Molecular cloning of the murine homologue of CD63/ME491 and			
RT	detection of its strong expression in the kidney and activated			
RT	macrophages";			
RL	Biochim. Biophys. Acta 1217:312-316(1994).			

RP	SEQUENCE FROM N.A.
RC	STRAIN=FVB/N; TISSUE=Mammary gland;
EX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA	Alschul S.F., Zeeberg B., Suecaw K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore I., Wax S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.B., Schetz T.B.,
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA	Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.C.N., Kzyvinski M.I., Skalska U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play some role in signal transduction pathways.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC -!- TISSUE SPECIFICITY: Strongly expressed in kidney.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC or send an email to license@isb-sib.ch).
CC

CC EMBL; D16432; BAA03904.1; -
CC EMBL; BC008108; AAH08108.1; -
CC EMBL; BC012212; AAH12212.1; -
CC PIR; S43511; S43511.
CC MGD; MGI:99529; Cd63.
CC InterPro: IPR000301; Transmem 4.
CC Pfam; PF00335; transmembrane4; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Glycoprotein; Antigen; Transmembrane; Lysosome.
CC INIT MET 0 BY SIMILARITY.
CC DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 11 31 POTENTIAL.
CC DOMAIN 32 50 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 51 69 POTENTIAL.
CC DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 81 106 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 107 202 POTENTIAL.
CC TRANSMEM 203 223 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 224 237 POTENTIAL.
CC CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 237 AA; 3C6BF1687B2A01C CRC64;
SQ

Query Match 13.9%; Score 227.5; DB 1; Length 237;
Best Local Similarity 27.8%; Pred. No. 1,7e-12;
Matches 68; Conservative 48; Mismatches 109; Indels 21; Gaps 8;

QY 2 AREDSVKLCRLCLLYALNLLFLWLSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYPP 61
DB 1 AVEGKMKCVKFLIYVLLAFACAVGLIAGVAVQVLKQAIT-----HETTAGSLIP 53
QY 62 VHPVMAVCCFLIIVGMGLGCTVKRNLLLAWFGLSVLIFCVELACGVTWYQELMV 121
DB 54 V--VTVAVGAFLLVAFVGGCCGACKENYCLMITFAIFLSLIMLVEVAIAIAGYVFRDQV 110
QY 122 PVQMSDWTLKARMTYGLPRYRWLTHAWNFFOREKCCGVVYFTDMLWEM--DWPPD 179
DB 111 KSEFNK--SFQOQMNQY-LKDNKAT-ILDKQKNNCCGASNTDWNIPGMKDRVDP 166
QY 180 SCCVREFFPGCSKQAHQEDLSLYQEGCGKMYSLFRTGKQLQVLRFLGISIGVTQILMI 239
DB 167 SCCINITVGGNDFKE--STHTQCGVEITAIWLR--KNILLVAAAGIAFVEVLGI 221
QY 240 LTTLL 245
DB 222 FSCCLV 227

RESULT 15

ID CD9_PIG STANDARD; PRT; 225 AA.

AC Q8WMQ3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CD9 antigen.
GN CD9.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Yubero N., Barbano M.J., Llanes D., Garrido J.J.;
RT "Molecular cloning of the pig homolog of tetraspanin CD9 antigen";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: INVOLVED IN PLATELET ACTIVATION AND AGGREGATION (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC

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CC or send an email to license@isb-sib.ch).
CC

CC EMBL; AY072785; AAL68966.1; -
CC InterPro: IPR008952; Tetraspanin.
CC InterPro: IPR000301; Transmem 4.
CC Pfam; PF00335; transmembrane4; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Glycoprotein; Antigen; Transmembrane; Lipoprotein.
CC INIT MET 0 BY SIMILARITY.
CC DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 12 32 POTENTIAL.
CC DOMAIN 33 52 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 53 73 POTENTIAL.
CC DOMAIN 74 84 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 85 108 POTENTIAL.
CC DOMAIN 109 192 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 193 218 POTENTIAL.
CC DOMAIN 219 225 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 225 AA; 25070 MW; FF280FE39BC11545 CRC64;
SQ

Query Match 13.4%; Score 220.5; DB 1; Length 225;
Best Local Similarity 25.0%; Pred. No. 6.5e-12;
Matches 66; Conservative 45; Mismatches 86; Indels 67; Gaps 9;

QY 8 KCLRLCLLYALNLLFLWLSISVLAVSAMRDYLNVLTLTAETR---VEEAVILTYFPVH 64
DB 7 KCIRKYLFGFNFIWLAGIAVLAIGLWLR-----FDSQTKSIFQENNNNSFYTGIV 58
QY 65 PVMAVCCFLIIVGMGLGCTVKRNLLLAWFGLSVLIFCVELACGVTWYQELMV 124
DB 59 -ILIGAGALMMVVGFLCCGAVGSCQCMGLGFFGLVIFAIETAAAIWYSHKQVKE 117
QY 125 WSDMV-----TLKARNTYGLPRYRWLTHAWNFFOREKCCGVVYFTDW 168
DB 118 VQDFYRDTYNKLGKDDPQRETLXA--IHVAL-----DCCGLMGEVQ 158
QY 169 LEMTEMDDPPSCCVREFFPGCSKQAHQEDLSLYQEGCGKMYSLFRTGKQLQVLRFLGI 228
DB 159 L-----LADICPQDV-----LSSLPKPCPEAIKEVFQ--NKFHIIAGVI 198
QY 229 SIGVTQILAMILITLLWALYDR 252
DB 199 GIADVMIFGMIFSMILCCAIRSR 222

Search completed: May 13, 2004, 16:06:11

Wed May 19 15:09:11 2004

us-09-830-328c-2.rsp

Page 12

Job time : 12.3363 secs

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:03:45 ; Search time 17.8142 Seconds
(without alignments)
883.899 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKLCRLLYALNLL.....IPEHTSMANSFNTHPEMEL 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCUS COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286	17.4	253	3 US-09-333-599-4	Sequence 4, Appli
2	286	17.4	253	4 US-09-499-781-4	Sequence 4, Appli
3	280	17.1	253	3 US-09-333-599-2	Sequence 2, Appli
4	280	17.1	253	4 US-09-499-781-2	Sequence 2, Appli
5	268	16.3	236	3 US-08-705-771-19	Sequence 19, Appl
6	268	16.3	236	4 US-09-417-540-19	Sequence 19, Appl
7	242.5	14.8	280	2 US-08-855-140-1	Sequence 1, Appli
8	237.5	14.5	267	3 US-08-430-225A-20	Sequence 20, Appl
9	232.5	14.2	265	2 US-08-807-044-1	Sequence 1, Appli
10	215.5	13.1	228	1 US-08-408-222B-1	Sequence 1, Appli
11	214.5	13.1	227	1 US-08-254-493-1	Sequence 1, Appli
12	214.5	13.1	227	2 US-08-253-751-6	Sequence 6, Appli
13	214.5	13.1	227	2 US-08-453-925-6	Sequence 6, Appli
14	214.5	13.1	227	4 US-08-403-253A-6	Sequence 6, Appli
15	214.5	13.1	227	4 US-08-435-816A-6	Sequence 6, Appli
16	204	12.4	237	3 US-08-808-148-3	Sequence 3, Appli
17	204	12.4	237	4 US-09-376-594-216	Sequence 216, App
18	193.5	11.8	219	2 US-08-855-140-4	Sequence 4, Appli
19	176	10.7	204	4 US-09-149-476-429	Sequence 429, App
20	175.5	10.7	281	3 US-08-808-148-4	Sequence 4, Appli
21	174.5	10.6	219	2 US-08-855-140-3	Sequence 3, Appli
22	174.5	10.6	219	2 US-08-807-044-3	Sequence 3, Appli
23	174.5	10.6	219	5 PCT-US91-04986-2	Sequence 2, Appli
24	163.5	10.0	252	3 US-08-705-771-17	Sequence 17, Appl
25	163.5	10.0	252	4 US-09-417-540-17	Sequence 17, Appl
26	148.5	9.0	241	3 US-08-808-148-1	Sequence 1, Appli
27	148.5	9.0	241	3 US-09-020-956-114	Sequence 114, App

28	148.5	9.0	241	3	US-09-030-607-114	Sequence 114, App
29	148.5	9.0	241	4	US-09-439-313-114	Sequence 114, App
30	148.5	9.0	241	4	US-09-352-616A-114	Sequence 114, App
31	148.5	9.0	241	4	US-09-232-149A-114	Sequence 114, App
32	148.5	9.0	241	4	US-09-159-812-114	Sequence 114, App
33	148.5	9.0	241	4	US-09-636-215-114	Sequence 114, App
34	148.5	9.0	241	4	US-09-685-166A-114	Sequence 114, App
35	148.5	9.0	241	4	US-09-115-453-114	Sequence 114, App
36	148.5	9.0	241	4	US-09-688-489-114	Sequence 114, App
37	148.5	9.0	260	3	US-08-957-130-15	Sequence 15, Appl
38	145.5	8.9	233	4	US-09-148-545-137	Sequence 137, App
39	142	8.6	245	4	US-09-482-273-133	Sequence 133, App
40	123	7.5	258	3	US-08-957-130-13	Sequence 13, Appl
41	98.5	6.0	123	4	US-09-149-476-693	Sequence 693, App
42	98.5	6.0	336	4	US-09-716-129-62	Sequence 62, Appl
43	90	5.5	418	1	US-08-194-338-9	Sequence 9, Appli
44	89	5.4	417	3	US-08-430-286A-12	Sequence 12, Appl
45	89	5.4	417	5	PCT-US91-00909-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-333-599-4
; Sequence 4, Application US/09333599
; Patent No. 6245898
; GENERAL INFORMATION:
; APPLICANT: Testa, Jacqueline E.
; APPLICANT: Quigley, James P.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
; FILE REFERENCE: SUNY
; CURRENT APPLICATION NUMBER: US/09/333,599
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PPT
; ORGANISM: Mus musculus
US-09-333-599-4

Query Match	17.4%;	Score 286;	DB 3;	Length 253;
Best Local Similarity	28.8%;	Pred. No. 2.3e-22;		
Matches	74;	Conservative	47;	Mismatches 96;
				Indels 40;
				Gaps 9;
QY	9	CIRCLLYALNLLFWMSISVLASAWRDYNNVLTATRTVEEAVILYFPVHPVMI	68	
Db	15	CKYLLFTYNCFFWLAGLVMAVGITLAKSDYISLASS-----TYLATAY-ILV	65	
QY	69	AVCCFLIIVGMLGYCGTVKRNLLLLAWPGSLIVFCVELACGWVYEQELMVPVQWSDM	128	
Db	66	VAGVVMVTVGLGCCATFKERNLLRLYFILLIIFLEIIAGILAYVQCLNTE----	121	
QY	129	VTLKARNTNYGLPYRWLTH-----ANFTQREPKCGVYFTDLENTMDW-----	176	
Db	122	--LKENLKDTWVKRYHQSGHEGVSSAVDKLQEPHCQGSNNSDW---QDSEWTRSGEAD	176	
QY	177	---PDPSCVREFPGCKQAQHQEDLSLY--QECGCKMYSFRLGKTKOLOVRLFLGISG	231	
Db	177	SRVPDSCCKTWNAGCKGRDH---ASNIYKVEGCITKLTFTIQ--EHLRVIGAVGIGIA	231	
QY	232	VTQILAMLTITLLWAL	248	
Db	232	CVQVFGMIFTCCLYRSL	248	
RESULT 2				
US-09-499-781-4				
; Sequence 4, Application US/09499781				
; Patent No. 6498014				

; GENERAL INFORMATION:
 ; APPLICANT: Testa, Jacqueline E.
 ; APPLICANT: Quigley, James P.
 ; APPLICANT: Seandel, Marco
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
 ; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
 ; FILE REFERENCE: SUNY
 ; CURRENT APPLICATION NUMBER: US/09/499,781
 ; CURRENT FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: 09/333,599
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-499-781-4

Query Match 17.4%; Score 286; DB 4; Length 253;
 Best Local Similarity 28.8%; Pred. No. 2.3e-22;
 Matches 74; Conservative 47; Mismatches 96; Indels 40; Gaps 9;
 QY 9 CLRLYALNLLFWLMSISVLAVSAMRDYLNKLVLTATETRVVEAVILTYPPVHPVMI 68
 DB 15 CLKYLLFTYNCFFWLAGLAVAGIWTALKSDYISLLASS-----TYLATAY-ILV 65
 QY 69 AVCCFLIIVGMGYCTGVRKRNLLLLAWYFGSLIVFCVELACGV--WTYEOELMVPVQMS 128
 DB 66 VAGVWVMTGVLGCCATFKERRNLLRLYFILLIIFLEIIAGILAYAYYQQLNTE---- 121
 QY 129 VTLKARMT-NYGLPRYRLTHAMNFFOREFKCCGVVYFTDWMLEMTDMW----- 176
 DB 122 --LKENLKTMTKRYHQPCHAEVTSVDLOQOEFFHCCGNSNSQDW---QDSEWIRSEAGGR 176
 QY 177 ---PPDSCCVREPPGCKQAHOEDLSLY--QEGCGKMYSLRGTQKQLVRLFGISIG 231
 DB 177 SRVVPDSCCKTVMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIA 231
 QY 232 VTQILAMILTITLLMAL 248
 DB 232 QVFGMIFTCCLYRSL 248

RESULT 3
 US-09-333-599-2
 ; Sequence 2, Application US/09333599
 ; Patent No. 6245898
 ; GENERAL INFORMATION:
 ; APPLICANT: Testa, Jacqueline E.
 ; APPLICANT: Quigley, James P.
 ; APPLICANT: Seandel, Marco
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
 ; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
 ; FILE REFERENCE: SUNY
 ; CURRENT APPLICATION NUMBER: US/09/333,599
 ; CURRENT FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-333-599-2

Query Match 17.1%; Score 280; DB 3; Length 253;
 Best Local Similarity 29.8%; Pred. No. 1e-21;
 Matches 76; Conservative 46; Mismatches 97; Indels 36; Gaps 10;
 QY 9 CLRLYALNLLFWLMSISVLAVSAMRDYLNKLVLTATETRVVEAVILTYPPVHPVMI 68
 DB 15 CLKYLLFTYNCFFWLAGLAVAGIWTALKSDYISLLASG-----TYLATAY-ILV 65

QY 69 AVCCFLIIVGMGYCTGVRKRNLLLLAWYFGSLIVFCVELACGV--WTYEOELMVPVQMS 126
 DB 66 VAGVWVMTGVLGCCATFKERRNLLRLYFILLIIFLEIIAGILAYAYYQQLNTEK-- 123
 QY 127 DMVTLKARMT-NYGLPRYRLTHAMNFFOREFKCCGVVYFTDWMLEMTDMW----- 176
 DB 124 --ENLKDVTMTKRYHQPCHAEVTSVDLOQOEFFHCCGNSNSQDW---RDSEWIRSEAGGR 178
 QY 177 ---PPDSCCVREPPGCKQAHOEDLSLY--QEGCGKMYSLRGTQKQLVRLFGISIGVT 233
 DB 179 WVPDSCCKTVMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233
 QY 234 QILAMILTITLLMAL 248
 DB 234 QVFGMIFTCCLYRSL 248

RESULT 4
 US-09-499-781-2
 ; Sequence 2, Application US/09499781
 ; Patent No. 6498014
 ; GENERAL INFORMATION:
 ; APPLICANT: Testa, Jacqueline E.
 ; APPLICANT: Quigley, James P.
 ; APPLICANT: Seandel, Marco
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
 ; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
 ; FILE REFERENCE: SUNY
 ; CURRENT APPLICATION NUMBER: US/09/499,781
 ; CURRENT FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: 09/333,599
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-499-781-2

Query Match 17.1%; Score 280; DB 4; Length 253;
 Best Local Similarity 29.8%; Pred. No. 1e-21;
 Matches 76; Conservative 46; Mismatches 97; Indels 36; Gaps 10;
 QY 9 CLRLYALNLLFWLMSISVLAVSAMRDYLNKLVLTATETRVVEAVILTYPPVHPVMI 68
 DB 15 CLKYLLFTYNCFFWLAGLAVAGIWTALKSDYISLLASG-----TYLATAY-ILV 65
 QY 69 AVCCFLIIVGMGYCTGVRKRNLLLLAWYFGSLIVFCVELACGV--WTYEOELMVPVQMS 126
 DB 66 VAGVWVMTGVLGCCATFKERRNLLRLYFILLIIFLEIIAGILAYAYYQQLNTEK-- 123
 QY 127 DMVTLKARMT-NYGLPRYRLTHAMNFFOREFKCCGVVYFTDWMLEMTDMW----- 176
 DB 124 --ENLKDVTMTKRYHQPCHAEVTSVDLOQOEFFHCCGNSNSQDW---RDSEWIRSEAGGR 178
 QY 177 ---PPDSCCVREPPGCKQAHOEDLSLY--QEGCGKMYSLRGTQKQLVRLFGISIGVT 233
 DB 179 WVPDSCCKTVMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233
 QY 234 QILAMILTITLLMAL 248
 DB 234 QVFGMIFTCCLYRSL 248

RESULT 5
 US-08-705-771-19
 ; Sequence 19, Application US/08705771
 ; Patent No. 6054289
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji.
 ; APPLICANT: Jian Ni and Jing-Shan Hu
 ; TITLE OF INVENTION: Human Genes, Sequences and

TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-771-19

Query Match 16.3%; Score 268; DB 3; Length 236;
Best Local Similarity 27.0%; Pred. No. 1.8e-20;
Matches 70; Conservative 45; Mismatches 98; Indels 46; Gaps 7;
QY 1 MAREDSVKRCILLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVVEAVILTYF 60
DB 1 MARA-CLQAVKYLMPAFNLFWLGGCVGLGVGLWLAQQGSFATLSS-----F 48
QY 61 PVVHP--VMIAVCCFLIIVGMGLYCGTVKRNLLLLAWYFGLLVIFCVF--LACGVWVYE 116
DB 49 PSLWAANLLIITGAFVMAIGFVGLGAIKENKCLLTLFFLLLLVFLLEGTTAILFFAYT 108
QY 117 QELMVPVQMSDMVTLKARMTNYGLPRYRWLTHANFFQREFKCCGVVYFTDMLWEMDM 176
DB 109 DKIDRYAQD---LKKGLHLYGTQGNVGLTNAWSIIQTDFRCGGSNVTDFEVYNATR 164
QY 177 PPDSCCVREPPGCKQAQHDLSLDLYQEGCKKMYSLRG-----TKQLQVLRFLG 227
DB 165 VPDSCCLE-----FSESCLHAPALVEGRATRGEGVASGELLAVGIFG 207
QY 228 ISIGVTQILAMILTITLLW 246
DB 208 LCTALVQILGLNFAMTYW 226

RESULT 6
US-08-705-771-19
Sequence 19, Application US/09417540
Patent No. 6639052
GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Honglin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,540
FILING DATE: 14-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF-96)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-417-540-19
Query Match 16.3%; Score 268; DB 4; Length 236;
Best Local Similarity 27.0%; Pred. No. 1.8e-20;
Matches 70; Conservative 45; Mismatches 98; Indels 46; Gaps 7;
QY 1 MAREDSVKRCILLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVVEAVILTYF 60
DB 1 MARA-CLQAVKYLMPAFNLFWLGGCVGLGVGLWLAQQGSFATLSS-----F 48
QY 61 PVVHP--VMIAVCCFLIIVGMGLYCGTVKRNLLLLAWYFGLLVIFCVF--LACGVWVYE 116
DB 49 PSLWAANLLIITGAFVMAIGFVGLGAIKENKCLLTLFFLLLLVFLLEGTTAILFFAYT 108
QY 117 QELMVPVQMSDMVTLKARMTNYGLPRYRWLTHANFFQREFKCCGVVYFTDMLWEMDM 176
DB 109 DKIDRYAQD---LKKGLHLYGTQGNVGLTNAWSIIQTDFRCGGSNVTDFEVYNATR 164
QY 177 PPDSCCVREPPGCKQAQHDLSLDLYQEGCKKMYSLRG-----TKQLQVLRFLG 227
DB 165 VPDSCCLE-----FSESCLHAPALVEGRATRGEGVASGELLAVGIFG 207
QY 228 ISIGVTQILAMILTITLLW 246
DB 208 LCTALVQILGLNFAMTYW 226

RESULT 7
US-08-855-140-1
Sequence 1, Application US/08855140
Patent No. 5854022
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/855,140
 FILING DATE: Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0296 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: MYOMNOT01
 CLONE: 779308
 US-08-855-140-1

Query Match 14.8%; Score 242.5; DB 2; Length 280;
 Best Local Similarity 27.4%; Pred. No. 1.2e-17;
 Matches 61; Conservative 35; Mismatches 90; Indels 37; Gaps 6;
 QY 9 CLRLLYALNLLFWLMSISVLAVSAMRDYLNKLVLTATETRVBEAVILTYPPVHP--V 66
 DB 8 CLKYMFELNLFWLCGGLGGINLSVSGNFATFPS-----FPSLSAANL 56
 QY 67 MIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGLSLVIFCVLACGVTYVEQLMVPV--- 123
 DB 57 VIAIGTIVMTGFLGCLGAIKENKCLLSFFIVLV-----TILAEILILPILFF 105
 QY 124 QKSDMTV-----LKARMTNYGLPRYRLTHAWNPFREFKCCGVVYFTDLEMTMDWP 177
 DB 106 VYMDKVENAKDLKEGLLYITENNVLGNKAWNLIQAEKCCGVTDYTDYFVLGENTV 165
 QY 178 PSCCVREPPFGCKQAQHEDLSDLYOEGCGCKMYFLRGTKOL 220
 DB 166 PDRCCMNSQGGGRNG-----TTPLRWTGCKXKXKXWFDNDKHV 204

RESULT 8
 US-08-430-225A-20
 Sequence 20, Application US/08430225A
 Patent No. 6204000
 GENERAL INFORMATION:
 APPLICANT: Dong, Jin-Tang; Barrett, J. Carl; Lamb, Patricia W.; Isaacs, John T.
 TITLE OF INVENTION: DIAGNOSTIC METHODS AND
 TITLE OF INVENTION: GENE THERAPY USING REAGENTS DERIVED FROM THE
 TITLE OF INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAI1
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/430,225A
 FILING DATE: 28-APR-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4172
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY:
 US-08-430-225A-20

Query Match 14.5%; Score 237.5; DB 3; Length 267;
 Best Local Similarity 27.0%; Pred. No. 3.8e-17;
 Matches 71; Conservative 51; Mismatches 100; Indels 41; Gaps 10;
 QY 7 VKLRCLLYALNLLFWLMSISVLAVSAM---RDYLNKLVLTATETRVBEAVILTYFPV 62
 DB 6 IKVTYKFLFLNLIFFILGAVILGFGVWILADKSSISVLQTSSTSSLRMG-----AY--- 57
 QY 63 VHPVMIACVCCFLIIVGMLGYCGTVKRNLLLLAWYFGLSLVIFCVLACGVTYVEQLMVP 122
 DB 58 ---VFIVGAVTWMGLGCGIGAVNEVRCLLGLYFAFLGLILIAQVTAGALFYNNMKLK 114
 QY 123 VQMSDMVTLKARMTNYGLPRYRLTHAWNPFREFKCCGVVYFTDLEMT---MDWP--- 177
 DB 115 QEMGGIVTELIR--DYNSSREDSLDQAWDYVQAVKCCGWVSYNNTDNLNMRPEVY 172
 QY 178 PSCCVR-----EPPGCKQA--HQEDLSLDLYOEGCGCKMYFLRGTKOLQ 221
 DB 173 PCSCVEGEEDNSLVKRGCEAPGNRTSGNHPEDW--PVYQEGCKMKVQAWLQ--ENLG 229
 QY 222 VLRFPLGISIGVTOILAMILTITL 244
 DB 230 IILGVGVVAIIELLGNVLSICL 252

RESULT 9
 US-08-807-044-1
 Sequence 1, Application US/08807044
 Patent No. 5863735
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/807,044
 FILING DATE: Herewith

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,493
FILING DATE: 06-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0224 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SCORNOT01
CLONE: 663655
US-08-807-044-1

Query Match 14.2%; Score 232.5; DB 2; Length 265;
Best Local Similarity 24.4%; Pred. No. 1.3e-16;
Matches 68; Conservative 47; Mismatches 103; Indels 61; Gaps 8;

QY 1 MAREDSVKLCRLCYALNLLFLWMSISVLAVSNMWDYLNVLTLTAETRVEEAVILTYF 60
DB 1 MAA-CLOAVKYLMPAFNLLFWGGCGVLGVGLWL-----AATGSGFATXSSSF 48
QY 61 PVVHP--VMTAVCCFLIIIVGMLGCGTVKRNLLLLAWYFGLIVFCVELACGVWYQOE 118
DB 49 PLSAANLLIITGAFVMAIGFVCGCJGAIKENKCLLTFTLLLLLVLENTAILLFF--- 105
QY 119 LMPVQWSDMV-----TLKARNTNGLPRYRLTHAWNFQR----- 155
DB 106 ----AYTKIDRYAQOQLKGLHLYGTQGNVGLTNWASIIQDXRGVGRWAGSAGAPSP 160
QY 156 -----EPKCCGVVFTDWMLEMTDMPDSCCVREFPGCSKQAHQEDLSLDYQEG 205
DB 161 XASARELAPQFRCGGSVNTDFEYVNAFVTRVDPDSCLEFSSCGLHAP-----GTWKAP 216
QY 206 CGKMYSFRLGTQKQVLRFLGISIGVTQILAMILITL 244
DB 217 CYETVKVWLQ--ENLLAVGIFGLCTALVQILGLTFAMTM 253

RESULT 10
US-08-408-222B-1
Sequence 1, Application US/08408222B
Patent No. 5776727
GENERAL INFORMATION:
APPLICANT: Ikeyama, Shuichi
APPLICANT: Koyama, Masaru
APPLICANT: Miyake, Masayuki
APPLICANT: Senoo, Masaharu
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,222B

FILING DATE: 22-MAR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,493
FILING DATE: 06-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-408-222B-1

Query Match 13.1%; Score 215.5; DB 1; Length 228;
Best Local Similarity 24.5%; Pred. No. 6.7e-15;
Matches 67; Conservative 44; Mismatches 93; Indels 69; Gaps 10;

QY 1 MAREDSVKLCRLCYALNLLFLWMSISVLAVSNMWDYLNVLTLTAETRVEEAVILTYF 60
DB 1 MPVKGTKICVILFGFNFIWLAGIYLAIGLRFDSQTKSIFEQETNNNS---SFY 57
QY 61 PVVHPVMTAVCCFLIIIVGMLGCGTVKRNLLLLAWYFGLIVFCVELACGVWY--EQE 118
DB 58 TGVY-ILIGAGALMVLVGLCGGAVQESQCMGLGFFGLVIFAIETAAIWIYSHKDE 116
QY 119 LMPVPQ--WSDMV-----TLKARNTNGLPRYRLTHAWNFQREFKCCGVVY 164
DB 117 VKEVQEFYKTYNKLTKDEPQRETLKA--IHYAL-----NCCGL-- 155
QY 165 FTDWLEMTENDWPP-----DSCCVREFPGCSKQAHQEDLSLDYQEGCKMYSFRLGTQK 219
DB 156 -AGVQEQTIDICPKKQVLETFVTKSCPDALKEVFD-----NKK 192
QY 220 LQVLRFLGISIGVTQILAMILITLLWALYYDR 252
DB 193 FHIIGAVGIGIYVAVVIMFIMFIMLCCAIRNR 225

RESULT 11
US-08-254-493-1
Sequence 1, Application US/08254493
Patent No. 5439886
GENERAL INFORMATION:
APPLICANT: IKEYAMA, SHUICHI
APPLICANT: KOYAMA, MASARU
APPLICANT: MIYAKE, MASAYUKI
APPLICANT: SENOO, MASAHARU
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-493-1

APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
APPLICANT: Freeman, Gordon J.
TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
PROLIFERATION OF T-CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-751-6

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160
QY 172 TENDWPP-----DSCCVREFFGCSKQAHQEDISDLYQEGCGKMYSLFRTGKQLQVLEFL 226
DB 161 FSDICFKKXDLVETFTFKSCPDARKEVFD-----NKFHIIIGAV 198
QY 227 GISIGVTOILAMILTTILLWALYYDR 252
DB 199 GIGIAVVMIFGMLFMSILCAIRNR 224

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160
QY 172 TENDWPP-----DSCCVREFFGCSKQAHQEDISDLYQEGCGKMYSLFRTGKQLQVLEFL 226
DB 161 FSDICFKKXDLVETFTFKSCPDARKEVFD-----NKFHIIIGAV 198
QY 227 GISIGVTOILAMILTTILLWALYYDR 252
DB 199 GIGIAVVMIFGMLFMSILCAIRNR 224

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160
QY 172 TENDWPP-----DSCCVREFFGCSKQAHQEDISDLYQEGCGKMYSLFRTGKQLQVLEFL 226
DB 161 FSDICFKKXDLVETFTFKSCPDARKEVFD-----NKFHIIIGAV 198
QY 227 GISIGVTOILAMILTTILLWALYYDR 252
DB 199 GIGIAVVMIFGMLFMSILCAIRNR 224

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160
QY 172 TENDWPP-----DSCCVREFFGCSKQAHQEDISDLYQEGCGKMYSLFRTGKQLQVLEFL 226
DB 161 FSDICFKKXDLVETFTFKSCPDARKEVFD-----NKFHIIIGAV 198
QY 227 GISIGVTOILAMILTTILLWALYYDR 252
DB 199 GIGIAVVMIFGMLFMSILCAIRNR 224

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160

Query Match 13.1%; Score 214.5; DB 1; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVBEAVILTFVFPVHPVM 67
DB 7 KCIKYLLFGFNFTFWLAGIAVLAIGLWLRFSQTSKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGCGTVKRNLLLAWVFGSLVIFCVELACGVWY--EQLMVPVQ- 124
DB 63 IGAGALMLVGLGCCGAVQESOCMLGLFFGLLVIFAFETIAAIAWYSHKDEVIKEVQ 122
QY 125 -WSDMV-----TLKASMTNYGLPRYRWLTHAMNFFQREKCCGVVYFTDWLEM 171
DB 123 FYKDTYNKLTQDEPQRETLKA--IHVAL-----NCCGL---AGGVEQ 160
QY 172 TENDWPP-----DSCCVREFFGCSKQAHQEDISDLYQEGCGKMYSLFRTGKQLQVLEFL 226
DB 161 FSDICFKKXDLVETFTFKSCPDARKEVFD-----NKFHIIIGAV 198
QY 227 GISIGVTOILAMILTTILLWALYYDR 252
DB 199 GIGIAVVMIFGMLFMSILCAIRNR 224

Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;

QY 172 TEMDWP-----DSCCVREFFPGCSKQAHQEDLSLYOEGCGKMYSLRGTKQLQVRL 226
Db 161 FISDICKVDLETFVTKSPDAIKEVDF-----NKPHIIGAV 198

QY 227 GISIGVTOILAMILTITILWALYYDR 252
Db 199 GIGIAVVMIFGMIFSMILCCAIRNR 224

RESULT 13
US-08-453-925-6
Sequence 6, Application US/08453925
Patent No. 5883223
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennett, Paul D., Freeman, Gordon J.
TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
PROLIFERATION OF T-CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,925
FILING DATE: 30 MAY 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253,751
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CPB
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-925-6

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;

Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;

QY 8 KCLRLIYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYFFVHVHM 67
Db 7 KCIIKYLFGFNFIWLAGIATGLMLRPSQTKSIFEQETNNNS---SFYTGVI-IL 62

QY 68 IAVCCFLIIVCMGLYCGTVKXENLLLLAWYFGSILVIFCVELACGWY--EQELMVPVQ- 124
Db 63 IGAGALMMLVGLGCCGAVQSCQMLGLFFGLLVIFAIEIAAAIANGYSHKDEVIKEVQE 122

QY 125 -WSDMV-----TLKARMTNYGLPRYRWLTHAWNPFQREFKCCGVVYFTDWMLE 171
Db 123 FYKTYNKLTKDEPQRETLKA--IHYAL-----NCCGL---AGGVEQ 160

QY 172 TEMDWP-----DSCCVREFFPGCSKQAHQEDLSLYOEGCGKMYSLRGTKQLQVRL 226
Db 161 FISDICKVDLETFVTKSPDAIKEVDF-----NKPHIIGAV 198

QY 227 GISIGVTOILAMILTITILWALYYDR 252
Db 199 GIGIAVVMIFGMIFSMILCCAIRNR 224

RESULT 14
US-08-403-253A-6
Sequence 6, Application US/08403253A
Patent No. 6352694
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennett, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-253A-6

Query Match 13.1%; Score 214.5; DB 4; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;
QY 8 KCLRCLLIYALNLLFWMISVLAWSAMRDYLNVLTLTAETRVEEAVILTYPPVHPVM 67
DB 7 KCIKYLFGNFIFWLAGIAVLAIGLWLRFDSTQKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVWY--EQELMVPVQ- 124
DB 63 IGAGALMWLVGFLGCCGAVQESOCMLGFLFGLVIFAIEIAAINGYSHKDEVIKEVQE 122
QY 125 -WSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQRFKCCGVVYFTDWMLE 171
DB 123 FYKDTYNKLTQDEPORETLKA--IHYAL-----NCCGL---AGGVEQ 160
QY 172 TEMDWP-----DSCCVREFPGCSKQAHQEDLSLDYQEGCGKMYSLRGTKQLQVLRL 226
DB 161 FISDICKKDVLETFYTKSCPDALKEVFD-----NKFHIIGAV 198
QY 227 GISIGVTCILAMLTITLLWALYDR 252
DB 199 GIGIAVMVFMIFSMILCCAIRNR 224

RESULT 15

US-08-435-816A-6
Sequence 6, Application US/08435816A
Patent No. 6534055

GENERAL INFORMATION:

APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994

APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-816A-6

Query Match 13.1%; Score 214.5; DB 4; Length 227;

Best Local Similarity 24.8%; Pred. No. 8.5e-15;

Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;

QY 8 KCLRCLLIYALNLLFWMISVLAWSAMRDYLNVLTLTAETRVEEAVILTYPPVHPVM 67
DB 7 KCIKYLFGNFIFWLAGIAVLAIGLWLRFDSTQKSIPEQETNNNS---SFTYGVY-IL 62
QY 68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVWY--EQELMVPVQ- 124
DB 63 IGAGALMWLVGFLGCCGAVQESOCMLGFLFGLVIFAIEIAAINGYSHKDEVIKEVQE 122
QY 125 -WSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQRFKCCGVVYFTDWMLE 171
DB 123 FYKDTYNKLTQDEPORETLKA--IHYAL-----NCCGL---AGGVEQ 160
QY 172 TEMDWP-----DSCCVREFPGCSKQAHQEDLSLDYQEGCGKMYSLRGTKQLQVLRL 226
DB 161 FISDICKKDVLETFYTKSCPDALKEVFD-----NKFHIIGAV 198
QY 227 GISIGVTCILAMLTITLLWALYDR 252
DB 199 GIGIAVMVFMIFSMILCCAIRNR 224

Search completed: May 13, 2004, 16:09:02

Job time : 18.8142 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: May 13, 2004, 16:02:15 ; Search time 14.5752 Seconds
(without alignments)
2012.897 Million cell updates/sec
Title: US-09-830-328c-2
Perfect score: 1642
Sequence: 1 MAREDSVKLCRLLYALNLL.....IFPHTSMANSFNTHFEMEEL 305
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	260.5	15.9	238	1 JC2297	CD63 antigen - rab
2	259.5	15.8	238	2 A59265	tetraspan TSPAN-4
3	255.5	15.6	238	1 I38016	melanoma-associate
4	242.5	14.8	238	1 A46508	CD63/MS491 antigen
5	237.5	14.5	267	1 A46493	metastasis suppress
6	232.5	14.2	238	1 S43511	CD63/MS491 antigen
7	220	13.4	206	2 T25161	hypothetical prote
8	215.5	13.1	228	1 A40402	CD9 antigen [valid
9	214.5	13.1	286	1 JX0221	CD9 antigen - bovi
10	213.5	13.0	228	1 A42929	CD9 antigen - gree
11	212.5	12.9	226	2 I49589	antigen - mouse
12	211.5	12.9	226	1 S39262	CD9 antigen - rat
13	204	12.4	237	1 A36056	tumor-associated a
14	199	12.1	236	1 A35649	cell surface prote
15	193	11.7	226	1 A46472	cell surface prote
16	192.5	11.7	281	1 A47629	cell surface glyco
17	191	11.6	244	1 I39368	T-cell acute lymph
18	187	11.4	245	2 A59258	tetraspan TSPAN-6
19	184.5	11.2	219	1 A39574	leukocyte antigen
20	184	11.2	253	2 A59264	tetraspan TSPAN-3
21	182.5	11.1	282	2 T21696	hypothetical prote
22	180	11.0	222	2 A59263	tetraspan TSPAN-2
23	178	10.8	245	2 A59260	tetraspan TSPAN-6
24	175	10.7	266	2 I49561	C33/R2/IA4 - mouse
25	174.5	10.6	219	1 A37243	hemopoietic cell s
26	171.5	10.4	281	1 B47629	cell surface glyco
27	164.5	10.0	218	1 A43522	23K integral memb
28	162	9.9	284	2 A59261	tetraspan TSPAN-5
29	158	9.6	359	2 T18667	hypothetical prote

ALIGNMENTS

RESULT 1

JC2297
CD63 antigen - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C:Accession: JC2297
R:Sonma, Y.; Suzuki, T.; Sasano, H.; Nagura, H.; Nose, M.; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A:Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanabe heritab
A:Reference number: JC2297; MUID:95120837; PMID:7820873
A:Accession: JC2297
A:Molecule type: mRNA
A:Residues: 1-238 <SOH>
A:Cross-references: DDBJ:D21264; NID:9684973; PIDN:BAA04804.1; PID:9684974
A:Experimental source: aorta
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein, lysosome, surface antigen, transmembrane protein
F:1-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>
F:52-76/Domain: transmembrane #status predicted <CY2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-103/Domain: transmembrane #status predicted <TM3>
F:104-202/Domain: extracellular #status predicted <EX2>
F:203-238/Domain: transmembrane #status predicted <TM4>
F:229-238/Domain: intracellular #status predicted <CY3>
F:125,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 260.5; DB 1; Length 238;
Best Local Similarity 30.0%; Pred. No. 3.3e-16;
Matches 74; Conservative 44; Mismatches 108; Indels 21; Gaps 7;
QY 1 MAREDSVKLCRLLYALNLLFLWMSISVLAVSANWRDYLNVLTLTAEIVVEAVILTYF 60
DB 1 MAVEGGMKVKFLLYLLAFACACAVGLIAGVGAQVLVSQIT- - - - -HGATPPGSL 53
QY 61 FVHPVMIACCFLLIIVGMLGCGTVKRNLLLLAWYFGSLIVFCVLACGVWYVEQLM 120
DB 54 PV- - -VIIVAGAFLLVAFVCGCGCKENYCLMITFAFLSLIMLVEVAIAAGVPRDK 110
QY 121 VVQMSDMVTLKARNTNYGLPRYRWLTHANFPREFKCCGVVFTDWNLETEM- -DWPP 178
DB 111 VMSEFNK- -DFRQOMQNYSTDNQAL- -ILDRMKDFTCCGAANYTDWATPGMTRDVP 166
QY 179 DSCCVREPPGCKQAQHELDLDYCEGGCKMYSFLLGTQKQLQVLRFLGIGIVTQILAM 238
DB 167 DSCCVNTSGGVKFP- - -NVKDIIVGCVKIGIWLNR- - -KNLVVAAALGIAFVVLGI 221
QY 239 ILITILL 245
DB 222 VFACCLV 228

uroplakin lb - bov
23K integral membr
hypothetical prote
tetraspan TSPAN-1
hypothetical prote
sarcoma amplified
hypothetical prote
hypothetical prote
TGFbeta-regulated
hypothetical prote
uroplakin Ia - bov
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

179 DSCCVREFPCCSKQAHOEDSLDYQEGCGKMYSLRGTQKQVLRFLGISIGVTOILAM 238
167 DSCCINTVGGCINFEK---AIHKEGCVKGGWLR--KNVLVVAARALGARFEVLGI 221
239 ILTITLL 245
222 VFACCLV 228
RESULT 4
A46508
CD63/ME491 antigen homolog - rat
N;Alternate names: mast cell antigen AD1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: A46508; S16776
C;Nishikata, H.; Oliver, C.; Mergenhagen, S.E.; Siraganlian, R.P.
J. Immunol. 149, 862-870, 1992
A;Title: The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen ME491)
A;Reference number: A46508; MUID:92340890; PMID:1634775
A;Accession: A46508
A;Molecule type: mRNA
A;Residues: 1-238 <NIS>
A;Cross-references: EMBL:X61654; NID:G55601; PIDN:CAA43935.1; PID:G55602
A;Note: This antigen was found localized to mast cells in tissue samples, but was induced by antigen extracted from NCBI backbone (NCBI:109346, NCBIP:109349)
C;Comment: This heavily glycosylated protein of 50-60K (27K after deglycosylation) is found on the surface of mast cells.
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; mast cell; surface antigen; transmembrane protein
F;1-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX2>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;130,150,172/Binding site: carbohydrate (Asn). (covalent) #status predicted

Query Match 14.8%; Score 242.5; DB 1; Length 238;
Best Local Similarity 28.7%; Pred. No. 1.4e-14;
Matches 73; Conservative 46; Mismatches 100; Indels 35; Gaps 9;
QY 1 MAREDSVKURCLLYALNLLFWLMSISVLAVSWMDYLNVLTLTAETRVBEAVILTF 60
DB 1 MAVEGGKVKVFLLYVLLAFCAVGLIAIGAVQVVLKQAIT-----HETTAGSL 53
QY 61 PVVHPVMIAYCCFLIIYVGMILGYCGTVKRNLLLLAWYFGSLVIFCVELACGVWVYQELM 120
DB 54 PV---VVIAGAFLLVAFVGCACAKENYCLMITFAIFSLIMLVEVAIAIGYVFRDQ 110
QY 121 VPVQMSDMVTLKAMTYNGLPRYRWLTH-----ANFFQREFKCGGVYFTDWMLEMT- 174
DB 111 VKSEFSK--SFQKQMQNY-----LTDNKTATILDKLENKCCGASNYTDWERIPGNA 161
QY 175 -DWPPDSCCVREFPCCSKQAHOEDSLDYQEGCGKMYSLRGTQKQVLRFLGISIGV- 232
DB 162 KDRVPDSCCINTVGGCNDPKF---STHTQGCVTETAAWLR---KNVLVVAAGAALGIA 214
QY 233 -TOILAMILITLL 245
DB 215 FVEVLGIIFSCCLV 228
RESULT 5
A46493
metastasis suppressor KAI1 - human
N;Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; type
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: I38942; S16156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J.

Science 268, 884-886, 1995
A;Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p1
A;Reference number: I38942; MUID:95273964; PMID:7754374
A;Accession: I38942
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: EMBL:U20770; NID:G806805; PIDN:AAC50133.1; PID:G806806
R;Gaagitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homology
A;Reference number: S16156; MUID:91153380; PMID:1842498
A;Accession: S16156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <GAU>
A;Cross-references: EMBL:X53795; NID:G35832; PIDN:CAA37804.1; PID:G35833
A;Note: The authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, N.
J. Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leu
D9, CD37, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-239, MV, 242-267 <IMA>
A;Cross-references: GB:S48196; NID:G258294; PIDN:AAB23825.1; PID:G258295
A;Experimental source: T-cell line MOJUT-4
A;Note: sequence extracted from NCBI backbone (NCBIP:117149)
C;Genetics:
A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <EX1>
F;58-78/Domain: transmembrane #status predicted <TM2>
F;79-83/Domain: intracellular #status predicted <CY2>
F;84-108/Domain: transmembrane #status predicted <TM3>
F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 237.5; DB 1; Length 267;
Best Local Similarity 27.0%; Pred. No. 4.6e-14;
Matches 71; Conservative 51; Mismatches 100; Indels 41; Gaps 10;
QY 7 VKCLRLYALNLLFWLMSISVLAVSAW---RDYLNVLTLTAETRVBEAVILTFPV 62
DB 6 IKVTYFLLFNLIIIFILGAVILFGVWILADKSSFISVLOTSSSLANG-----AY--- 57
QY 63 VHPVMIAYCCFLIIYVGMILGYCGTVKRNLLLLAWYFGSLVIFCVELACGVWVYQELMVP 122
DB 58 ---VFVGVAVTLMAGELGCGAVNEVRCLLGLYFAFLLILIAQVTAGALFYFNMGLK 114
QY 123 VQVMSDMVTLKAMTYNGLPRYRWLTHANFFQREFKCGGVYFTDWMLEMT- MDWP---- 177
DB 115 QEMGGIVTELIR--DYNSSREDSLQDAWDYVQAVQKCGVSWFYNTWDAELNNPEVY 172
QY 178 PDSCCVR-----EFGCSKQA--HOEDSLDYQEGCGKMYSLRGTQKQJQ 221
DB 173 PCSCEVKGEEDNSLSVRKGFCEAPGNRTQSGNHPEDW-PVYQEGCMKVQAWLQ--ENLG 229
QY 222 VLRFIGISIGVTOILAMITLL 244
DB 230 IILGVGVVAITELLGVLISCL 252
RESULT 6

A:Reference number: S10564; MUID:90292223; PMID:2358073
A:Accession: S10564
A:Molecule type: protein
A:Residues: 2-8, 'X', 10-21 <HIG>
C:Genetics:
A:Gene: GDB:CD9; MTC3
A:Map position: 12p13-12p13
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.1%; Score 215.5; DB 1; Length 228;
Best Local Similarity 24.5%; Pred. No. 3.9e-12;
Matches 67; Conservative 44; Mismatches 93; Indels 69; Gaps 10;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVEEAVILTYF 60
DB 1 MPVKGTKCIKYLFGNFIFWLAGIAGLWLRFDSDQTKSIPEQETNNNS--SFY 57

QY 61 PVVHPVMAVCCFLIIVGMLGCGTVKRNLLLAWFGSLVIFCVELACGWYTY--EQE 118
DB 58 TGVY-ILIGAGALMLVGLGCCGAVQSCQMLGFFGLVFAIEIAAIAWGYSHKDE 116

QY 119 LMVYPVQ--WSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQREKCGGVY 164
DB 117 VKEVEFYKDYTNKLTWDEPQETLKA--HYAL-----NCCGL-- 155

QY 165 FTDWLEMTMDWPP-----DSCCVREFPGSKQAHQEDLSLYQEGCGKMYFLRGTKQ 219
DB 156 -AGGVQFQSDICPKXDLVETFTVKSQDAKEVFD-----NKK 192

QY 220 LQVLRFLGISGVTQILAMILITLWALYDR 252
DB 193 FHIIGAVGIGIAVWIFGWFMSILCAIRNR 225

RESULT 9
JX0221
CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C:Accession: JX0221
R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A:Reference number: JX0221; MUID:93054422; PMID:1339429
A:Accession: JX0221
A:Molecule type: mRNA
A:Residues: 1-226 <MAR>
A:Cross-references: GB:M81720; NID:G162820; PIDN:AAA30439.1; PID:G162821
A:Experimental source: ocular ciliary epithelial cell
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-226/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>

F:220-226/Domain: intracellular #status predicted <CY3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.1%; Score 214.5; DB 1; Length 226;
Best Local Similarity 24.3%; Pred. No. 4.7e-12;
Matches 67; Conservative 51; Mismatches 81; Indels 77; Gaps 13;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETR---VEEAVIL 57
DB 1 MPVKGTKCIKYLFGNFIFWLAGIAGLWLR-----FDSQTKSIPEQENNS 52

QY 58 TYPVHPVMAVCCFLIIVGMLGCGTVKRNLLLAWFGSLVIFCVELACGWYTY-- 115
DB 53 SFYTGTV-ILIGAGALMLVGLGCCGAVQSCQMLGFFGLVFAIEIAAIAWGYSH 111

QY 116 EQELMWVQ--WSDMVTLKARNTNYGLPRYRWLTHAWNFFQRE-----FKCCGVY-- 163
DB 112 KEVIVKEVQFYEDTYN--KLKNDPE-----QRETLKAIHALDCCGLTGV 156

QY 164 ---YFTDWLEMTMDWPP-----DSCCVREFPGSKQAHQEDLSLYQEGCGKMYFLRG 216
DB 157 PEQLTLD-----TCPKRLIDSLKTRPCP-----EADIEIFR----- 189

QY 217 TKQLQVLRFLGISGVTQILAMILITLWALYDR 252
DB 189 -SKFHIIGAVGIGIAVWIFGWFMSILCAIRNR 223

RESULT 10
A42929
CD9 antigen - green monkey
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C:Accession: A42929
R:McMamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
epitopes on toxin-sensitive cells
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-228 <MIT>
A:Cross-references: GB:D10726; NID:G218565; PIDN:BAA01569.1; PID:G218566
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52/53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.0%; Score 213.5; DB 1; Length 228;
Best Local Similarity 24.2%; Pred. No. 5.9e-12;
Matches 66; Conservative 45; Mismatches 93; Indels 69; Gaps 10;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVEEAVILTYF 60
DB 1 MPVKGTKCIKYLFGNFIFWLAGIAGLWLRFDSDQTKSIPEQETNNNS--SFY 57

QY 61 PVVHPVMAVCCFLIIVGMLGCGTVKRNLLLAWFGSLVIFCVELACGWYTY--EQE 118
DB 58 TGVY-ILIGAGALMLVGLGCCGAVQSCQMLGFFGLVFAIEIAAIAWGYSHKDE 116

QY 119 LMVYPVQ--WSDMV-----TLKARNTNYGLPRYRWLTHAWNFFQREKCGGVY 164

Db 117 VIREVQEFYKDTYNKLTKEPQRETLKA--IHVAL-----DCGGL-- 155
QY 165 FTDWLEMTEDWPP-----DSCCVREPPGSKQAHOEDLSLDYQEGCGKKMYSLRGTKQ 219
Db 156 -AGVVEQFISIDCPKQDVLETFIKCPDAKEVFD-----NK 192
QY 220 LOVLRFELIGSIGVTOILAMITITLLWALYDR 252
Db 193 FHIAGVIGIAVVMIFGMIFSMILCCAIRNR 225

RESULT 11
antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C:Accession: I49589
R:Rubinstein, E.; Ballard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: GB:I08115; NID:G388911; PIDN:AAA7405.1; PID:G388912
C:Superfamily: CD9 antigen

Query Match 12.9%; Score 212.5; DB 2; Length 226;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
Matches 65; Conservative 46; Mismatches 86; Indels 67; Gaps 10;

QY 8 KCLRCLLYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEATR---VEEAVILTFPPVH 64
Db 8 KCILYLLFGFNFIWLAGIAVLAIGLWLR-----FDSQTKSIFEQETHSSFTYGVY 59

QY 65 PVMIACVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVW--TYEQELMVP 122
Db 60 -ILIGAGALMVLVGLGCCGAVQESQCMGLGFFGLVIFAIETIAAAVWGYTHKDEVKE 118

QY 123 VQ--WSDMV--TLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWM 168
Db 119 LOEFYKDTYQKLSKDEPQRETLKA-----IHMLDCCGI---AGP 156

QY 169 LEWTEWDWPPDSCVREPPGSKQAHOEDLSLDYQEGCGKKMYSLRGTKQLQVLRFLGI 228
Db 157 LEQFISDTCPKQKOLLESP---QVKPCPEAISEVF-----NNKPHIIGAVGI 199

QY 229 SIGVTOILAMITITLLWALYDR 252
Db 200 GIAVVMIFGMIFSMILCCAIRNR 223

RESULT 12
CD9 antigen - rat
N:Alternate names: platelet cell surface glycoprotein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C:Accession: S39262
R:Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A:Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in a variety of tissues.
A:Reference number: I56562; MUID:95123481; PMID:7823164
A:Accession: I56562
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: EMBL:X76489; NID:G434314; PIDN:CAA54027.1; PID:G434315
C:Genetics:
C:Gene: CD9
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein

F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-80/Domain: transmembrane #status predicted <TM2>
F:81-84/Domain: intracellular #status predicted <CY2>
F:85-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CY3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 211.5; DB 1; Length 226;
Best Local Similarity 25.4%; Pred. No. 8.9e-12;
Matches 64; Conservative 46; Mismatches 99; Indels 43; Gaps 10;

QY 8 KCLRCLLYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEATR---VEEAVILTFPPVH 64
Db 8 KCILYLLFGFNFIWLAGIAVLAIGLWLR-----FDSQTKSIFEQETHSSFTYGVY 59

QY 65 PVMIACVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLVIFCVELACGVW--TYEQELMVP 122
Db 60 -ILIGAGALMVLVGLGCCGAVQESQCMGLGFFGLVIFAIETIAAAVWGYTHKDEVKE 118

QY 123 VQ--WSDMV--TLKARMTNYGLPRYRWLTHAWNFFQREKCCGVVYFTDWMLEMDPPDS 180
Db 119 LOEFYKDTY---QKLRNKDEPQRETL---KAHMLNCCGI---AGGVEQFISDTCPK 168

QY 181 CCVREPPGSKQAHOEDLSLDYQEGCGKKMYSLRGTKQLQVLRFLGISIGVTOILAMIL 240
Db 169 QVLESP-----QVKSCPAIDEVHSEKH-----IIGAVGIGIAVVMIFGMIF 211

QY 241 TITLLWALYDR 252
Db 212 SMILCCAIRNR 223

RESULT 13
A36056
tumor-associated antigen CO-029 - human
C:Species: Homo sapiens (man)
C>Date: 16-Nov-1990 #sequence_revision 09-Aug-1996 #text_change 20-Apr-2000
C:Accession: A36056
R:Szala, S.; Kasai, Y.; Stepelwski, Z.; Rodeck, U.; Koprowski, H.; Linnenbach, A.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6833-6837, 1990
A:Title: Molecular cloning of cDNA for the human tumor-associated antigen CO-029 and identification of its complementary DNA sequence.
A:Reference number: A36056; MUID:90370878; PMID:2395876
A:Molecule type: mRNA
A:Residues: 1-237 <SZA>
A:Cross-references: GB:M35252; NID:G180925; PIDN:AAA35709.1; PID:G180926
C:Genetics:
A:Gene: GDB:TM4SF3
A:Cross-references: GDB:9113496; OMIM:600769
C:Superfamily: CD9 antigen
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-33/Domain: transmembrane #status predicted <TM1>
F:34-52/Domain: extracellular #status predicted <EX1>
F:53-78/Domain: transmembrane #status predicted <TM2>
F:79-82/Domain: intracellular #status predicted <CY2>
F:83-107/Domain: transmembrane #status predicted <TM3>
F:108-205/Domain: extracellular #status predicted <EX2>
F:206-232/Domain: transmembrane #status predicted <TM4>
F:233-237/Domain: intracellular #status predicted <CY3>
F:37,118/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.4%; Score 204; DB 1; Length 237;
Best Local Similarity 25.5%; Pred. No. 4.5e-11;
Matches 64; Conservative 53; Mismatches 92; Indels 42; Gaps 12;

QY 9 CLRCLLYALNLLFWLMSISVLAVSAMWRDYLNNVLTLTAEATR---EEAVILTFPPVH 64
Db 7 CIKYSMTFNFLWLCGLIILALAIWR-----VSNDSQAIFGSEVDGSSIVAV-- 56

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: May 13, 2004, 16:01:35 ; Search time 39.4071 Seconds
(without alignments)
2442.024 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKLCRLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	99.6	305	4 Q8N3Y0	Q8N3Y0 homo sapien
2	1615	98.4	305	11 Q8BKT6	Q8BKT6 mus musculus
3	1611	98.1	305	11 Q8BZU1	Q8BZU1 mus musculus
4	1111.5	67.7	301	13 Q7N2G0	Q7N2G0 brachydanio
5	287	17.5	253	11 Q921J7	Q921J7 mus musculus
6	280	17.1	253	4 Q86U54	Q86U54 homo sapien
7	274.5	16.7	239	11 Q8BUJ2	Q8BUJ2 mus musculus
8	257.5	15.7	238	13 Q7SY95	Q7SY95 xenopus lae
9	252	15.3	253	11 Q9D1D1	Q9D1D1 mus musculus
10	240.5	14.6	248	13 Q7ZW21	Q7ZW21 xenopus lae
11	238.5	14.5	267	4 Q7Z2D4	Q7Z2D4 homo sapien
12	237	14.4	227	13 Q7ZUH9	Q7ZUH9 brachydanio
13	232.5	14.2	249	11 Q8BT06	Q8BT06 mus musculus
14	225	13.7	232	5 Q9XV14	Q9XV14 caenorhabdi
15	224	13.6	215	4 Q8N6Z9	Q8N6Z9 homo sapien
16	217.5	13.2	228	13 Q8AV92	Q8AV92 petromyzon

17	216.5	13.2	224	13 Q9IBC9	Q9IBC9 gallus gall
18	214.5	13.1	226	6 Q8MJ48	Q8MJ48 sus scrofa
19	203	12.4	242	4 Q7Z5N2	Q7Z5N2 homo sapien
20	202	12.3	236	6 Q7YRE9	Q7YRE9 tupaia bela
21	202	12.3	249	13 Q7ZXL9	Q7ZXL9 xenopus lae
22	199	12.1	222	13 Q8AV91	Q8AV91 petromyzon
23	196	11.9	227	13 Q7SYR5	Q7SYR5 xenopus lae
24	196	11.9	236	11 Q91V78	Q91V78 mus musculus
25	194.5	11.8	236	13 Q7ZTR5	Q7ZTR5 xenopus lae
26	193.5	11.8	283	5 Q8MS10	Q8MS10 drosophila
27	191	11.6	244	4 Q7Z3K6	Q7Z3K6 homo sapien
28	191	11.6	244	6 Q7YQ10	Q7YQ10 pan troglod
29	190	11.6	239	5 Q9NB10	Q9NB10 manduca sex
30	190	11.6	244	6 Q7YQX9	Q7YQX9 pongo pygma
31	189.5	11.5	283	11 Q8R3S2	Q8R3S2 mus musculus
32	188.5	11.5	248	5 Q9VLH1	Q9VLH1 drosophila
33	187.5	11.4	268	5 Q9V3X2	Q9V3X2 drosophila
34	186.5	11.4	265	13 Q8O2B9	Q8O2B9 xenopus lae
35	186	11.3	235	11 Q8R3G9	Q8R3G9 mus musculus
36	185.5	11.3	283	4 Q86UF1	Q86UF1 homo sapien
37	185	11.3	251	13 Q7SXT2	Q7SXT2 brachydanio
38	184	11.2	235	11 Q55158	Q55158 rattus norv
39	184	11.2	236	13 Q9DD57	Q9DD57 brachydanio
40	182.5	11.1	282	5 Q19983	Q19983 caenorhabdi
41	182	11.1	245	11 Q8BPU2	Q8BPU2 mus musculus
42	181	11.0	253	11 Q80XR4	Q80XR4 mus musculus
43	180	11.0	204	11 Q8BTH3	Q8BTH3 mus musculus
44	180	11.0	240	11 Q99J59	Q99J59 mus musculus
45	178.5	10.9	267	5 Q9V3B5	Q9V3B5 drosophila

ALIGNMENTS

RESULT 1

Q8N3Y0 PRELIMINARY; PRT; 305 AA.
ID Q8N3Y0
AC Q8N3Y0; 01-OCT-2002 (TREMREL. 22, Created)
DT 01-OCT-2002 (TREMREL. 22, Last sequence update)
DE 01-JUN-2003 (TREMREL. 24, Last annotation NET-2)
DE Transmembrane 4 superfamily member tetraspan NET-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031265; AAH31265.1; -.
DR InterPro; IPR000301; Transmem.4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 305 AA; 35356 MW; EC57D5E13A8B92DC CRC64;

Query Match	99.6%;	Score 1536;	DB 4;	Length 305;
Best Local Similarity	99.7%;	Pred. No. 3e-152;		
Matches 304;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MAREDSVKLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETREEAVILTYF	60	
Db	1	MAREDSVKLCRLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETREEAVILTYF	60	
QY	61	PVVHPVMIACVCFLLIVGMLGCGYGVKKNLLLLAWYFGSLVIFCVELACGWTVEQELM	120	
Db	61	PVVHPVMIACVCFLLIVGMLGCGYGVKKNLLLLAWYFGSLVIFCVELACGWTVEQELM	120	
QY	121	VPVQSDVVTLLKARMTNYGLPRYRLTHAWNFFQREKCCGVVYFTDLEMTMDWPPDS	180	
Db	121	VPVQSDVVTLLKARMTNYGLPRYRLTHAWNFFQREKCCGVVYFTDLEMTMDWPPDS	180	

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszynski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC054563; A4H54563.1; -
RW Hypothetical protein.
SQ SEQUENCE 301 AA; 34093 MW; C4CDA310F298C200 CRC64;

Query Match 67.7%; Score 1111.5; DB 13; Length 301;
Best Local Similarity 66.9%; Pred. No. 8.7e-101;
Matches 208; Conservative 40; Mismatches 46; Indels 17; Gaps 4;

QY 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSWMDYLNVLTLTAETRVVEAVILTYF 60
DB 1 MAREDSVKLCRLCYALNLLFWLMSISVLAVSWMDYLNVLTLTAETRVVEAVILTYF 60

QY 61 PVVHPVVIACVCLITVGMGCGYGVKRNLLILAWFVGLVIFVFCVELACGVVYEQELM 120
DB 61 PVVHPVVIACVCLITVGMGCGYGVKRNLLILAWFVGLVIFVFCVELACGVVYEQELM 120

QY 121 VPVOWSDMTLKARMTNYGLPRYRWLTHAWNFFQRFKCGVYFTDWMLEMTDPPDS 180
DB 120 --VORSMDISLGRMPHFLQRYQLWTHAWNQLTELKCGVYFTDWMLEMTDPPDS 177

QY 181 CCVREPPGCKSQAHQEDSLDYOECCGCKMYSLRGTQLOVRLRELIGISIGVTOILAMTL 240
DB 178 CCNQVPGCARQAHYNDLSLYOECCGCKMYSLRGTQLOVRLRELIGISIGVTOILAMTL 237

QY 241 TITLLWALYDRREP---GTDQMSLKNDSQHLSCPSVELLKPSLSRIFETSMAV--- 294
DB 238 TVTLLWALYDHRKPPBPASADALI-----HTHSPTEDPLKVSHPRASEAWANTPA 289

QY 295 SFNTHFEMEEL 305
DB 290 NGHTQFEMEQL 300

RESULT 5
Q921J7 ID Q921J7 PRELIMINARY; PRT; 253 AA.
AC Q921J7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to CD151 antigen.
GN CD151.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012236; A4H12236.1; -
DR MGD; MGI:1096360; CD151.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 253 AA; 28241 MW; A4BEFB049253C311 CRC64;

Query Match 17.5%; Score 287; DB 11; Length 253;
Best Local Similarity 29.5%; Pred. No. 5.8e-20;
Matches 75; Conservative 48; Mismatches 97; Indels 34; Gaps 9;

QY 9 CLRCCLLYALNLLFWLMSISVLAVSWMDYLNVLTLTAETRVVEAVILTYFPVHPVMI 68
DB 15 CLKLYLLFYNCFFWLAGVAVGWITLAKSDYISLLASG-----TYLATAY-ILV 65

QY 69 AVCCFLITVGMGCGYGVKRNLLILAWFVGLVIFVFCVELACGV--WTYEQELMVPVQWS 126
DB 66 VAGVVMVTVGLGCCATFKERNLLRLYFILLIIFLEIIAGILAYVYQQLNTELEK 125

QY 127 DMVTLKARMTNYGLPRYRWLTHAWNFFQRFKCGVYFTDWMLEMTD--- 176
DB 126 LKDTMVKRYHQSG--HEGVTSADVQLQEFHCSCGNSQDW---QDSEWHSGEADSRV 179

QY 177 PPDSCCVREPPGCKSQAHQEDSLDY--OEGCGCKMYSLRGTQLOVRLRELIGISIGVTO 234
DB 180 VPDSCCKTNVAGCGKRDH--ASNIYKVGCGITLKTFFIQ--EHLRVIGAVGIGIACVQ 234

QY 235 ILAMILITITLWAL 248
DB 235 VFGMIFTCCLYRSL 248

RESULT 6
Q86U54 ID Q86U54 PRELIMINARY; PRT; 253 AA.
AC Q86U54;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD151 antigen.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BT007397; AAP36061.1; -
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 253 AA; 28295 MW; 0C8FE4CF2C3C286D CRC64;

Query Match 17.1%; Score 280; DB 4; Length 253;
Best Local Similarity 29.8%; Pred. No. 2.8e-19;
Matches 76; Conservative 46; Mismatches 97; Indels 36; Gaps 10;

QY 9 CLRCCLLYALNLLFWLMSISVLAVSWMDYLNVLTLTAETRVVEAVILTYFPVHPVMI 68
DB 15 CLKLYLLFYNCFFWLAGVAVGWITLAKSDYISLLASG-----TYLATAY-ILV 65

QY 69 AVCCFLITVGMGCGYGVKRNLLILAWFVGLVIFVFCVELACGV--WTYEQELMVPVQWS 126
DB 66 VAGVVMVTVGLGCCATFKERNLLRLYFILLIIFLEIIAGILAYVYQQLNTELEK-- 123
RP SEQUENCE FROM N.A.

QY 127 DMVTLKARMT-NYGLPRYRWLTHANWFFQBPFCCKGCVVYFTDWMLEMTMDW-----176
 Db 124 --ENLKDITMKRYHQPGHEAVTSVADQLQCPHCSCGNNNSQDM---RDSEWIRSQEAGGR 178
 QY 177 -PDSCCVREFPCCSKQAQOEDSLDY--CEGGCKKMYSLRGTKQLQVLRFLGIGISGVT 233
 Db 179 VPDSCCKTVVALLCGQRD---ASNIYKVEGGCITKLEFIQ--EHLRVIGAVGIGIACV 233
 QY 234 QILAMILITITLLWAL 248
 Db 234 QVFGMIFTCCLYRSL 248

RESULT 7

Q8BUJ2 PRELIMINARY; PRT; 239 AA.
 AC Q8BUJ2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Tetraspan NET-5 homolog (Hypothetical protein).
 GN 9430079M16RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The RIKEN Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK079139; BAC37559.1; --
 DR EMBL; BC052503; AAH52503.1; --
 DR MGD; MGI:1924558; 9430079M16RIK.
 DR InterPro: IPR000301; Transmem_4.
 DR Pfam: PF00335; Transmembrane4; 1.
 DR PRINTS; PRO0259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Hypothetical protein.

SQ SEQUENCE 239 AA; 26737 MW; B3DC47ADA1D877DD CRC64;
 Query Match 16.7%; Score 274.5; DB 11; Length 239;
 Best Local Similarity 29.2%; Pred. No. 9.1e-19;
 Matches 74; Conservative 40; Mismatches 110; Indels 29; Gaps 7;
 QY 9 CIRCILLAL---NLLFWLMSISVLAVSANWEDYLNVLTLTAETRVEEAVILYFVVPVHP 65
 Db 5 CLCCKYTMFENLFWLGGGLGVLGWSVSGNFATFSPS-----FPLSA 53
 QY 66 --VMIAVCCFLIIIVMLGCGCTVARNLLILLAWYFGLVIFPCVELACGVTYFQELMPV 123
 Db 54 ANLVIAIGTIVMTGFLGCLGAIKENKCLLSFFVILLIILLABELLIILFF--VYMDKV 111
 QY 124 QMSDMVTLKARMTNYGLPRYRWLTHANWFFQBPFCCKGCVVYFTDWMLEMTMDWPPDSCCV 183
 Db 112 NENAKQDLKEGLLYNTENNVLGNWNIQAEMRCGCVTDYTDWYFVLGENTVDPDCCM 171
 QY 184 REFPCSKQAQOEDSLDYOEQGGCKMYSLRGTKQLQVLRFLGIGISGVTQIILAMILITIT 243
 Db 172 ENSGCGENS---TTPMRTGTCYKVKLWFDNKK--HVLGTVMCILINQILGMAFSMT 225
 QY 244 LLWALY-----YD 251
 Db 226 LFOHIRTGKKYD 238

RESULT 8

Q7SY95 PRELIMINARY; PRT; 238 AA.
 AC Q7SY95;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Colon, Eye, and Skin;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the Riken Genome Exploration Research Group Phase I & II Team;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054957; AAH54957.1; -
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 325757 MW; 032D4D875A2A4F7D CRC64;

Query Match 15.7%; Score 257.5; DB 13; Length 238;
Best Local Similarity 25.0%; Pred. No. 4.2e-17;
Matches 62; Conservative 58; Mismatches 105; Indels 23; Gaps 7;

QY 1 MAREDSVKLCRLCYALNLLFLWMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYF 60
DB 1 MAYEGGKCKVCLNFFNFVWCGIALIAGIYVQIQLNHTLMKNAASSGAPIVV-- 57
QY 61 PVHPVMVAVCCFLIIIVGMLGYCGTVKRNLLLLAWYFGLSVLPCVELACGVWYVQELM 120
DB 58 -----IVGVGVIFLI--AFFGCGALKENYCMVTTFAVLVLVFLVEIAAAIAYYKDK 110
QY 121 VPVQWSDMVLTKARMTNYGLPRYRWLTHANFFOREFKCCGVVFTDWLE--MTEDWDP 177
DB 111 LRTAFED--SFKNGMSKNTTKD--ITESIDLLQKEFKCCGAFTNDWKQYPPFNGTDAV 166
QY 178 PDSCCVREFPFGCSKQAHQEDLSLYQEGCGKMYFLRGTKQLQVLRFLGISIGVQTILA 237
DB 167 PDSCKTIIAGCGK---DPSATINTDGCATGIDQWYK--KNIGIVAGVALGIALFEILG 220
QY 238 MILTITLL 245
DB 221 IIFACCLM 228

RESULT 9
Q9D1D1 PRELIMINARY; PRT; 253 AA.
ID Q9D1D1 PRELIMINARY; PRT; 253 AA.
AC Q9D1D1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1110014F12Rik protein (Weakly similar to platelet-endothelial
DE tetraspan antigen 3).
GN 1110014F12Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fleischer C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Suzuki H., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Wyszewski B.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 403:685-690 (2001).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon, Eye, and Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
RL Nature 420:563-573 (2002).
DR EMBL; AK003691; BAB22942.1; -
DR EMBL; AK028808; BAC26129.1; -
DR EMBL; AK033788; BAC35523.1; -
DR EMBL; AK090022; BAC41051.1; -
DR MGD; MGI:1915748; 1110014F12Rik.
DR InterPro; IPR000301; Transmem. 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 253 AA; 28072 MW; 8A820157A945C60A CRC64;

Query Match 15.3%; Score 252; DB 11; Length 253;
Best Local Similarity 29.6%; Pred. No. 1.6e-16;
Matches 73; Conservative 40; Mismatches 104; Indels 30; Gaps 8;

QY 10 LRCLLYALNLLFLWMSISVLAVSAMRDYLNVLTLTAETRVVEAVILTYFVHPVMA 69
DB 16 LKYLFIFFPFWVGAAVAVGIW-----TLVEKSGYLSILASSTPAASAYILIF 66
QY 70 VCCFLIIIVGMLGYCGTVKRNLLLLAWYFGLSVLPCVELACGV--WTYQELMVPVQWSD 127
DB 67 VGGVMTTGFLGFGAIIREQKSLSTYFCLLIVFLVELVAGVLAVHYQRLSDELKWH- 125
QY 128 MYTLKARMT-NYGLPRYRWLTHANFFOREFKCCGVVFTDWLEMTM-----DWPPD 179
DB 126 ----LNSTTFHYGQPRAAEITASVDRLOQDFKCCGNSADWQHSAYILSQEALGRQYVD 182
QY 180 SCCVREFPFGCSKQAHQEDLSLY--QEGCGKMYFLRGTKQLQVLRFLGISIGVQTILA 237
DB 183 SCKTIVARCGORAHF--SNIIYKVEGCGMAKLEQFV--ADHLLMGVAGVIGVACLCICG 237
QY 238 MILTITLL 244
DB 238 MVLTCCCL 244

RESULT 10
Q7ZWZ1 PRELIMINARY; PRT; 248 AA.
ID Q7ZWZ1 PRELIMINARY; PRT; 248 AA.
AC Q7ZWZ1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CD63 antigen (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RC Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC046575; AAH46575.1; -
DR InterPro; IPR000301; Transmem. 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
FT NON TER 1
SQ SEQUENCE 248 AA; 27115 MW; DC1801E256C7B6B6 CRC64;

Query Match 14.6%; Score 240.5; DB 13; Length 248;
Best Local Similarity 24.2%; Pred. No. 2.1e-15;
Matches 61; Conservative 55; Mismatches 105; Indels 31; Gaps 7;

QY 1 MAREDSVKLCRLCLLVALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVBEAVILTYF 60
 Db 9 MAVSGGKCVKFLNFFNFVFWGCIALIAIGIVQIQNHTLMKNATSSGTFPI-----63
 QY 61 PVHPVMIACCCFLIIIVGMLGYCGTVKRNLLLLAWFGSLIVFCVELAGV--WTYEQE 118
 Db 64 -----AIIIVGLVIFLIAFFCCGALKENYCMVTFPAVLVILFLVBEIAAIAAYVKOK 118
 QY 119 LWPVQVSDMVTLKARMTNYGLPYRWLTHANFFOREFKCCGVYFTDWMLEMDWP- 177
 Db 119 LRTAFES-----FKDGMRSYN--NTRKEMADSIDLLQKFEKCCGAFNSTDKQVAPFVGT 172
 QY 178 --PDSCCVREPFGGSKQAQHDLSLDYQEGCGKMYSLFRGTQKQLVRLFGISIGVTOI 235
 Db 173 NVPDSCCKNITAGCGKAPFP--NSINTDGCANGIDQWVK-----KNIGIVAGVALG 222
 QY 236 LAMILITITLLWA 247
 Db 223 IALFETLGIIPA 234

RESULT 11

Q722D4 PRELIMINARY; PRT; 267 AA.
 ID Q722D4
 AC Q722D4
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Kangai 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marz M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX Strausberg R.;
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX Strausberg R.;
 RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000726; AAH00726.1;
 DR EMBL; BC001821; AAH01821.1;
 SQ SEQUENCE 267 AA; 29611 MW; FC3786A4521CABDE CRC64;

Query Match 14.58; Score 238.5; DB 4; Length 267;
 Best Local Similarity 27.04; Pred. No. 3.5e-15;

Matches 71; Conservative 51; Mismatches 100; Indels 41; Gaps 10;
 QY 7 YKLCRLCLLVALNLLFWLMSISVLAVSAMW-----RDYLNVLTLTAETRVBEAVILTYFV 62
 Db 6 IKVTYFLEFLNLFILGAVILGFGWILADKSSFSISVLTQSSSRMG-----AY---57
 QY 63 VHPVMIACCCFLIIIVGMLGYCGTVKRNLLLLAWFGSLIVFCVELAGVWVYQELMVP 122
 Db 58 ---VFIGVAVTLMGLFGCGICGAVNEVRCCLGLYFAFLLILLIAQVTAGALFYENMGK 114
 QY 123 VQMSDMVTLKARMTNYGLPYRWLTHANFFOREFKCCGVYFTDWMLEMT-MDWP-----177
 Db 115 QEMGGIVTELIR--DYNSSREDSLDQAWDYVQAQKCCGWVSFYNTDNLAMRPEVY 172
 QY 178 PDSCCVR-----EFPCCSKQA--HODLSLDYQEGCGKMYSLFRGTQKQLQ 221
 Db 173 PCSCEVKGEEDNSLSVRKGFCEAFGNRTQSGNHPEDW-PVYQEGCMKVQAWLQ--ENLG 229
 QY 222 VLRFLGISIGVTOILAMITITL 244
 Db 230 IILGVGVGVAIVELLGMVLSICL 252

RESULT 12

Q7ZUH9 PRELIMINARY; PRT; 227 AA.
 ID Q7ZUH9
 AC Q7ZUH9
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RX Strausberg R.;
 RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC049036; AAH49036.1;
 DR InterPro; IPR008952; Tetraspanin.
 DR InterPro; IPR003101; Transmem. 4.
 DR Pfam; PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 24362 MW; A48ABBA2B74B100 CRC64;

Query Match 14.4%; Score 237; DB 13; Length 227;
 Best Local Similarity 28.9%; Pred. No. 4.1e-15;
 Matches 73; Conservative 42; Mismatches 100; Indels 38; Gaps 10;

QY 1 MAREDSVKLCRLCLLVALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVBEAVILTYF 58
 Db 1 NAAGGGLQCIKYLFIFFNFIWLAGTGLVAVGLWLRFDKTKPEFFTAEN--GQTVFLTV 58
 QY 59 YFPVHPVMIACCCFLIIIVGMLGYCGTVKRNLLLLAWFGSLIVFCVELAGVW--TYE 116
 Db 59 Y-----ILIVAGAMVMVVGELGCCGAIKESACMLGLFFMLLVIFAFAAAGIWLGNK 112
 QY 117 QELMVPVQMSDMVTLKARMTNYGLPYRWLTHANFFOREFKCCGVY-YFTDWMLEMTMD 175
 Db 113 DKIVSDVQOQFYTOIVKYNKESPDGFLKETLT-AIHF---SIQCGPTGLASDGVSVT---165
 QY 176 WPPDSCCVREPFGGSKQAQHDLSLDYQEGCGKMYSLFRGTQKQLVRLFGISIGVTOI 235
 Db 166 -----QEGLANVITTCGSSVIQDMF--NSLHVIGGVGIGIVIMV 207
 QY 236 LAMILITITLLWAL 248
 Db 208 FGMFSLMLCCAI 220

Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wild A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81128; CAB03397.2; -.
 DR FIR; T25161; T25161.
 DR WormPep; T23D8.2; CE26006.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 SQ SEQUENCE 232 AA; 25206 MW; 1073713036131492 CRC64;
 Query Match 13.7%; Score 225; DB 5; Length 232;
 Best Local Similarity 25.8%; Pred. No. 6.3e-14;
 Matches 64; Conservative 50; Mismatches 96; Indels 38; Gaps 9;
 QY 4 EDSVKRLCLLYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEEAVILTYFPV 63
 DB 3 EGVTVIKLFLFANLVLVWGSLIIVGSLIQLKFDNVLIDGLERLATPILL----- 56
 QY 64 HPVMIACVCFIIIVGMLGYCGTVKRNLLLLAWFGLSVIFCVLACGWTYEQELMPV 123
 DB 57 --LVIGSLCTLL--GFLGCGGAIRENYCLTVSFAVLLALLITCEIAAVIIGVALH----- 107
 QY 124 QMSDMVTLK-ARNTNYGLPRY---RWLTHANFFPREFKCCGVVFTDWMLEMDWDPD 179
 DB 108 ---DSFRLGIGNOLQTMVRYHESRGVSASWAKTKQLPECCGVTTSSDWLTFTTI---PD 161
 QY 180 SCVREFPGCSKQAHQEDLSLYQCGCKMYSFRLGTQKQLQVRLFLGISIGVTQILMI 239
 DB 162 SCIEHIEGAREN-----APLFEFGC-----IHSVEQ-WYLKNGAMVGICAVLAI 208
 QY 240 LITITLWA 247
 DB 209 QLVGVCF 216
 RESULT 15
 OX Q8N629 PRELIMINARY; PRT; 215 AA.
 ID Q8N629
 AC Q8N629;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Lysosome-associated membrane protein-3 variant.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Ancans J., Suzuki I., Thody A.J.;
 RT "Melanocyte variant of lysosome-associated membrane protein-3 (LAMP3);
 RT also CD63 and melanoma associated antigen ME419) mRNA";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF508304; AAM34259.1;
 DR GO; GO:0005615; C:extracellular space; IEA.
 DR GO; GO:0005386; F:carrier activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000264; Serum_albumin.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.

RESULT 13
 OX Q8BT06 PRELIMINARY; PRT; 249 AA.
 ID Q8BT06
 AC Q8BT06;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Cd63 antigen.
 GN CD63.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL; AK028220; BAC25821.1; -.
 DR MGD; MGI:995229; Cd63.
 DR GO; GO:0005615; C:extracellular space; IEA.
 DR GO; GO:0005386; F:carrier activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000264; Serum_albumin.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; transmembrane4; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00212; ALBUMIN; 1.
 DR PROSITE; PS00421; TW4.1; 1.
 SQ SEQUENCE 249 AA; 26784 MW; E2716D4FC9482443 CRC64;
 Query Match 14.2%; Score 232.5; DB 11; Length 249;
 Best Local Similarity 27.9%; Pred. No. 1.3e-14;
 Matches 69; Conservative 48; Mismatches 109; Indels 21; Gaps 8;
 QY 1 MAREDSVKRLCLLYALNLLFWLMSISVLAVSAMRDYLNVLTLTAETRVVEEAVILTYF 60
 DB 12 MAVEGGKCVKFLYLVLLACACAVGLIAGVAVQVVLQAII-----HETAGSLL 64
 QY 61 PVHPVMIACVCFIIIVGMLGYCGTVKRNLLLLAWFGLSVIFCVLACGWTYEQELM 120
 DB 65 PV---VIAVGAFLPLVAFVCGCGACKENYCLMITFAIFLSLMLVEVAIAAGYVFRDQ 121
 QY 121 VPQMSDMVTLKARNTNYGLPRYRWLTHANFFPREFKCCGVVFTDWMLEMDWDP 178
 DB 122 VKSEFNK--SFQQQMNQY-LKDNKTAI-ILDKLQENNCAGSYTTDWENIPGMKDRVP 177
 QY 179 DSCVREFPGCSKQAHQEDLSLYQCGCKMYSFRLGTQKQLQVRLFLGISIGVTQILAM 238
 DB 178 DSCCINIVGCGNDPKE---STIHTQGCVEITAIWL--KNILLVAAAALGIAFVEVLGI 232
 QY 239 ILTITLL 245
 DB 233 IFSCCLV 239
 RESULT 14
 OX Q9XVI4 PRELIMINARY; PRT; 232 AA.
 ID Q9XVI4
 AC Q9XVI4;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE T23D8.2 protein.
 GN T23D8.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiidae; Rhabditoidea;

DR PROSITE: PS00212; ALBUMIN; 1.
DR PROSITE: PS00421; TM4.1; 1.
SQ SEQUENCE 215 AA; 23430 MW; C4469E42BCC8C4F7 CRC64;
Query Match 13.6%; Score 224; DB 4; Length 215;
Best Local Similarity 26.7%; Pred. No. 7.3e-14;
Matches 66; Conservative 43; Mismatches 94; Indels 44; Gaps 7;
QY 1 MAREDSVKLCRLIYALNLLFWLMSISVLAYSANMRDYLNNVLTETATRVEEAVILTYF 60
Db 1 MAVEGGMKCVKFLLYVLLLAFC-----GATPGSL 30
QY 61 FVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLIVFCVELACGWMTYEQLM 120
Db 31 PV--VLIAGVFLFLVAFVCGCGACKENYCLMITFAIFLSLIMLVEVAALAGYVPRDK 87
QY 121 VPVQWSDMVTLLKARNTNYGLPRYRWLTHANFFOREFKCCGVYFTDWMLENTM--DWPP 178
Db 88 VMSEFNN--NFRQQMENY--PKNNHTASILDRLMQADFKCCGAANYTDWEKIPSMKRV 143
QY 179 DSCCVREPPGCKQAHOEDLSLDYCEGCGKMYSLRGTQLOVRLFLGISIGVTOILAM 238
Db 144 DSCCINVTGCGINFEK--AIHKGCVEKIGGLR--KNVLVVAALGIAFVEVLGI 198
QY 239 ILTITLL 245
Db 199 VFACCLV 205

Search completed: May 13, 2004, 16:07:37
Job time : 40.4071 secs

;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 86.58; Score 2393.8; DB 10; Length 2397;
Best Local Similarity 99.98; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 AGAGAAAGAGCGTCTCCAGCTGAAGCCCAATGAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
Db 1 AGAGAAAGAGCGTCTCCAGCTGAAGCCCAATGAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy 422 CCCTGCCCCGATGAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGCGTGGGCGAC 481
Db 61 CCCTGCCCCGATGAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGCGTGGGCGAC 120

Qy 482 CGGSCCCAGCGCCGACGATCGCTGCCGTTTGGCTTGGAGTAGATGGTGAAAGGA 541
Db 121 CGGSCCCAGCGCCGACGATCGCTGCCGTTTGGCTTGGAGTAGATGGTGAAAGGA 180

Qy 542 TGGGGCTTCTCCCTTACGGGGCTCAACAATGGCCAGAGAAATTCGCGAAGTCTCGCGC 601
Db 181 TGGGGCTTCTCCCTTACGGGGCTCAACAATGGCCAGAGAAATTCGCGAAGTCTCGCGC 240

Qy 602 TGCTGCTCTACGCCCTCAATCGCTCTTTGGTTAATGTCATCAGTGTTGGCAGTT 661
Db 241 TGCTGCTCTACGCCCTCAATCGCTCTTTGGTTAATGTCATCAGTGTTGGCAGTT 300

Qy 662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db 301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy 722 GAGGACGAGTCATTTGACTTCTTCCCTGGTTCATCCGTCATGATTCGCTTTGTC 781
Db 361 GAGGACGAGTCATTTGACTTCTTCCCTGGTTCATCCGTCATGATTCGCTTTGTC 420

Qy 782 TGTTCCTTATCATTTGGGGATGTTAGGATATTGGACCGTGAAAGAAATCTGTTG 841
Db 421 TGTTCCTTATCATTTGGGGATGTTAGGATATTGGACCGTGAAAGAAATCTGTTG 480

Qy 842 CTTCTTGATGTTTGAAGTTTCTGTCATTTCTGTTAGAACCTGGCTTGTGGC 901
Db 481 CTTCTTGATGTTTGAAGTTTCTGTCATTTCTGTTAGAACCTGGCTTGTGGC 540

Qy 902 GTTTTGGACATATGAACAGGACTTATGGTTCAGTACAAATGGTCAGATATGTCATTG 961
Db 541 GTTTTGGACATATGAACAGGACTTATGGTTCAGTACAAATGGTCAGATATGTCATTG 600

Qy 962 AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGTTGGAAT 1021
Db 601 AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGTTGGAAT 660

Qy 1022 TTTTTCAGAGAGTTTAAAGTCTGGAGTAGTATATTTTCACTGACTGGTTGGAATG 1081
Db 661 TTTTTCAGAGAGTTTAAAGTCTGGAGTAGTATATTTTCACTGACTGGTTGGAATG 720

Qy 1082 ACAGAGATGGACTGGCCCCCAGATTCTGCTGCTGTTAGAGAAATCCAGGATGTTCCAAA 1141

Db 721 ACAGAGATGGACTGGCCCCCAGATTCTGCTGTTAGAGAAATCCAGGATGTTCCAAA 780

Qy 1142 CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAAAGAAATGTAT 1201

Db 781 CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAAAGAAATGTAT 840

Qy 1202 TCCTTTTGGAGGAAACCAAACTGCTGAGGTTTCTGGGAAATCCCAATGGG 1261

Db 841 TCCTTTTGGAGGAAACCAAACTGCTGAGGTTTCTGGGAAATCCCAATGGG 900

Qy 1262 GTGACACAAATCCTGGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321

Db 901 GTGACACAAATCCTGGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy 1322 AGAAGGAGCGGGGACAGACCAATGATGCTTGAAGATGACAACTCTCAGCACCTG 1381

Db 961 AGAAGGAGCGGGGACAGACCAATGATGCTTGAAGATGACAACTCTCAGCACCTG 1020

Qy 1382 TCATGCTCCTCAGTAGAAATGTTGAAACCAAGCCCTGTCAGAAATCTTTGAAACACACATCC 1441

Db 1021 TCATGCTCCTCAGTAGAAATGTTGAAACCAAGCCCTGTCAGAAATCTTTGAAACACACATCC 1080

Qy 1442 ATGGCAAAACAGCTTTTAAATACACATTTGAGATGAGAGGATTATAAAAGAAATGTACAG 1501

Db 1081 ATGGCAAAACAGCTTTTAAATACACATTTGAGATGAGAGGATTATAAAAGAAATGTACAG 1140

Qy 1502 AAGAAACCAACAACTCTGTTTACTGGACTTGTGAATTTTGGTACATATCTGTGTTT 1561

Db 1141 AAGAAACCAACAACTCTGTTTACTGGACTTGTGAATTTTGGTACATATCTGTGTTT 1200

Qy 1562 CAGAAATATGTAGAAATATAAATGTTGCCATAAATAACACCTAAGCATATCTATTCTA 1621

Db 1201 CAGAAATATGTAGAAATATAAATGTTGCCATAAATAACACCTAAGCATATCTATTCTA 1260

Qy 1622 TCCTTTAAATGAGGATGGAAGTTTTCATGTCATAGTCCACCCTCGACAAATATTGA 1681

Db 1261 TCCTTTAAATGAGGATGGAAGTTTTCATGTCATAGTCCACCCTCGACAAATATTGA 1320

Qy 1682 TGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGAGCTGTGTATGACTTTTA 1741

Db 1321 TGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGAGCTGTGTATGACTTTTA 1380

Qy 1742 CTGAACACAGTTATGTTTGGAGGAGATGTTGATTAGCATTTCCGCAATCCCATGAAA 1801

Db 1381 CTGAACACAGTTATGTTTGGAGGAGATGTTGATTAGCATTTCCGCAATCCCATGAAA 1440

Qy 1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAACTAGT 1861

Db 1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAACTAGT 1500

Qy 1862 ATATAAGTACTAAATTAATGCTAACATAGGAAGTTAGAAAATACTATAAATTTTATTA 1921

Db 1501 ATATAAGTACTAAATTAATGCTAACATAGGAAGTTAGAAAATACTATAAATTTTATTA 1560

Qy 1922 CTCAGGATCTATTTCTTCTGATGCTAAATAAATATATATCAGAAATCTTCAATATTGG 1981

Db 1561 CTCAGGATCTATTTCTTCTGATGCTAAATAAATATATATCAGAAATCTTCAATATTGG 1620

Qy 1982 TGACTACCTTAAATGTTGTTTCTGCTGTTACTTAAATAATTTCTTACCACTTAAAGAGCAA 2041

Db 1621 TGACTACCTTAAATGTTGTTTCTGCTGTTACTTAAATAATTTCTTACCACTTAAAGAGCAA 1680

Qy 2042 GCTAACATATGCTTAAAGCTGATCAGGATTTTGTATATAGTCTGTGTAAATCTG 2101

Db 1681 GCTAACATATGCTTAAAGCTGATCAGGATTTTGTATATAGTCTGTGTAAATCTG 1740

Qy 2102 TATAATTCAGTCGATTTTCTGATTAATGTTTGAAGATAACCATTTATGAAAGGAAAT 2161

Db 1741 TATAATTCAGTCGATTTTCTGATTAATGTTTGAAGATAACCATTTATGAAAGGAAAT 1800

Qy 2162 TTGCTCCTGTATAGCATCATTTTCTGCTTTCTGTTTAAATGAGCTTTACTATTCTGT 2221

Db 1801 TTGTCCTGTATGACATCAATTATTTTACGCTTTTCTGTATTAAGCTTTACTATTTCTGT 1860
Qy 2222 CCTGGGCTTATTTACACATATACTGTTATTTTAAATACCTTAACCACTAATTTTGAAAT 2281
Db 1861 CCTGGGCTTATTTACACATATACTGTTATTTTAAATACCTTAACCACTAATTTTGAAAT 1920
Qy 2282 TACCAGTGTGATACATAGGAATCATTTATTCAGAAATGAGTCTGGTCTTTAGGAAGTATTA 2341
Db 1921 TACCAGTGTGATACATAGGAATCATTTATTCAGAAATGAGTCTGGTCTTTAGGAAGTATTA 1980
Qy 2342 ATAGAAATTTGACATTAACCTAGTTAGTTGATTCAGAAAGGCTTTGATGCTTTTCTCC 2401
Db 1981 ATAGAAATTTGACATTAACCTAGTTAGTTGATTCAGAAAGGCTTTGATGCTTTTCTCC 2040
Qy 2402 CAAATGAAGACTCTTTTGTGACACTAAACACTTTTAAAGCTTATCTTTGCCCTTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTGTGACACTAAACACTTTTAAAGCTTATCTTTGCCCTTCTCCA 2100
Qy 2462 AACAGAAAGCAATAGTCTCCAAGTCAATATAAATCTACAGAAATAGTCTTTTCT 2521
Db 2101 AACAGAAAGCAATAGTCTCCAAGTCAATATAAATCTACAGAAATAGTCTTTTCT 2160
Qy 2522 CCAGAAATAGTCTGTGAGAAATCATTTAAACATGTCAGAAATTTAGAGATTTCTTTGTTTA 2581
Db 2161 CCAGAAATAGTCTGTGAGAAATCATTTAAACATGTCAGAAATTTAGAGATTTCTTTGTTTA 2220
Qy 2582 TTTCACTGATTAATATACTGTGGCAATTTACAGAAATTTAAATTTTACAGAGTA 2641
Db 2221 TTTCACTGATTAATATACTGTGGCAATTTACAGAAATTTAAATTTTACAGAGTA 2280
Qy 2642 TAGTATATTTATTTGAATCGGAAAGTGCATTTTACTGATTTTGTGATTTTGTAT 2701
Db 2281 TAGTATATTTATTTGAATCGGAAAGTGCATTTTACTGATTTTGTGATTTTGTAT 2340
Qy 2702 TTCTCAGAAATGGAAGAAATTTAAATGTGCAATTAATTTTCTAGAGAGTAA 2758
Db 2341 TTCTCAGAAATGGAAGAAATTTAAATGTGCAATTAATTTTCTAGAGAGTAA 2397

RESULT 2

US-10-015-395A-272
; Sequence 272, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830F1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 272
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-272
Query Match 86.5%; Score 2393.8; DB 12; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 362 AGAGAAAGAGCGTCTCCAGCTGAAGCAATGACGCCCTCCGGCTCTCCCGAAGAAAGTT 421
Db 1 AGAGAAAGAGCGTCTCCAGCTGAAGCAATGACGCCCTCCGGCTCTCCCGAAGAAAGTT 60
Qy 422 CCTGCCCCGATGAGACCCGCCCGCTGCTCCCGACTATCCCGAGGCGGGGCTGGGCGAC 481
Db 61 CCTGCCCCGATGAGACCCGCCCGCTGCTCCCGACTATCCCGAGGCGGGGCTGGGCGAC 120
Qy 482 CGGGCCAGCGCCGACGATCGCTCCCGTTTGGCCCTTGGGAGTAGGATGCTGTAAGGA 541
Db 131 CGGGCCAGCGCCGACGATCGCTCCCGTTTGGCCCTTGGGAGTAGGATGCTGTAAGGA 180
Qy 542 TGGGCTTTCTCCCTTACGGGCTCACAAATGGCCAGAGAAATCCGTGAAGTGTCTGGC 601
Db 181 TGGGCTTTCTCCCTTACGGGCTCACAAATGGCCAGAGAAATCCGTGAAGTGTCTGGC 240
Qy 602 TGCCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCATCAGTGTGTTGGCAGTT 661
Db 241 TGCCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCATCAGTGTGTTGGCAGTT 300
Qy 662 TCTGCTTGGATGAGGAGTACTTAAATAATGTTCTCACTTTAACTGAGAAACGAGGTA 721
Db 301 TCTGCTTGGATGAGGAGTACTTAAATAATGTTCTCACTTTAACTGAGAAACGAGGTA 360
Qy 722 GAGGAGCAGTCATTTGACTTACTTCTGCTGCTTCCATCGGTCATGATGCTGTTTGC 781
Db 361 GAGGAGCAGTCATTTGACTTACTTCTGCTGCTTCCATCGGTCATGATGCTGTTTGC 420
Qy 782 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGAACCGTGAAAGAAATCTCTTG 841
Db 421 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGAACCGTGAAAGAAATCTCTTG 480
Qy 842 CTTCCTGATCGTACTTTGGAAGTTTGTGTCATTTTCTGTGTAGAACTGGCTGTGGC 901
Db 481 CTTCCTGATCGTACTTTGGAAGTTTGTGTCATTTTCTGTGTAGAACTGGCTGTGGC 540
Qy 902 GTTTGGACATGAAACAGGAACTTATGTTCCAGTACAAATGTTGTCAGATATGTTGCTT 961
Db 541 GTTTGGACATGAAACAGGAACTTATGTTCCAGTACAAATGTTGTCAGATATGTTGCTT 600
Qy 962 AAAGCCAGGATGACAAATTTATGATTTACCTAGATATCGTGGCTTACTCATGTTGAAT 1021
Db 601 AAAGCCAGGATGACAAATTTATGATTTACCTAGATATCGTGGCTTACTCATGTTGAAT 660
Qy 1022 TTTTTCAGAGAGATTTTAACTGCTGCTGAGTATATTTCACTGACTGTTGGAAATG 1081
Db 661 TTTTTCAGAGAGATTTTAACTGCTGCTGAGTATATTTCACTGACTGTTGGAAATG 720
Qy 1082 ACAGAGATGAGTGGCCCCCAGATTTCTGCTGTGTAGAGAAATCCAGGATGTTCCAAA 1141
Db 721 ACAGAGATGAGTGGCCCCCAGATTTCTGCTGTGTAGAGAAATCCAGGATGTTCCAAA 780
Qy 1142 CAGGCCACAGGAAAGTCTCAGTGACCTTTATCAGAGGGTGTGGGAGAAATGAT 1201
Db 781 CAGGCCACAGGAAAGTCTCAGTGACCTTTATCAGAGGGTGTGGGAGAAATGAT 840
Qy 1202 TCTTTTTCAGAGAAACCAACAACTGCGAGTGTGAGTTTCTGCGAAATCTCCATTGGG 1261
Db 841 TCTTTTTCAGAGAAACCAACAACTGCGAGTGTGAGTTTCTGCGAAATCTCCATTGGG 900
Qy 1262 GTGACACAAATCTCTGGGCAATGTTCTCACCATTACTCTGCTGGGCTCTGTATTATGAT 1321
Db 901 GTGACACAAATCTCTGGGCAATGTTCTCACCATTACTCTGCTGGGCTCTGTATTATGAT 960
Qy 1322 AGAGGGAGCGGCGACAGCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG 1381
Db 961 AGAGGGAGCGGCGACAGCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG-1020
Qy 1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCTGTTCAAGATCTTTTGAACACACATCC 1441
Db 1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCTGTTCAAGATCTTTTGAACACACATCC 1080

Db 2221 TTTCACTGATTAAATACTGTGGCAAAATTACAGAGTATTAAATTTTTTACAGAGTA 2280
Qy 2642 TAGTATATTATTGAAATCGGAAAGTGCATTTTACTGTATTTTCTGTATTTTGTAT 2701
Db 2281 TAGTATATTATTGAAATCGGAAAGTGCATTTTACTGTATTTTGTATTTTGTAT 2340
Qy 2702 TTCTCAGATATCGAAGAAATATAAATGTGCAATAAATATTTTCTAGAGTA 2758
Db 2341 TTCTCAGATATCGAAGAAATATAAATGTGCAATAAATATTTTCTAGAGTA 2397

RESULT 4

US-10-199-670-323
; Sequence 323, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1Q401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO: 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 AGAAGAGAGCGTCTCCAGTGAAGCCATGACGCCCTCCGCTCTCCGCGAAGATT 421
Db 1 AGAAGAGAGCGTCTCCAGTGAAGCCATGACGCCCTCCGCTCTCCGCGAAGATT 60
Qy 422 CCCTGCCCGATGAGCCCGCCCGCTGCGTCCCGACTATCCAGCGCGCGCTGGGCGAC 481
Db 61 CCCTGCCCGATGAGCCCGCCCGCTGCGTCCCGACTATCCAGCGCGCGCTGGGCGAC 120

Qy 482 CGGCGCCAGCGCCGAGAGATCGCTCGCGTTTGGCCCTTGGGAGTAGGATGGTGAAGGA 541
Db 121 CGGCGCCAGCGCCGAGAGATCGCTCGCGTTTGGCCCTTGGGAGTAGGATGGTGAAGGA 180
Qy 542 TGGGCGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGAGATTCGGTGAAGTCTCGCG 601
Db 181 TGGGCGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGAGATTCGGTGAAGTCTCGCG 240
Qy 602 TGCGTGTCTACGCGCTCAATCTGCTCTTTTGGTAAATGTCATCAGTGTGTTGGCAGTT 661
Db 241 TGCGTGTCTACGCGCTCAATCTGCTCTTTTGGTAAATGTCATCAGTGTGTTGGCAGTT 300
Qy 662 TCTGCTGGATGAGGAGTACCTAAATAATGTTCTCACTTAACTGCAAGAACGAGGTA 721
Db 301 TCTGCTGGATGAGGAGTACCTAAATAATGTTCTCACTTAACTGCAAGAACGAGGTA 360
Qy 722 GAGGAAGCAGTCATTTTGAATTTTCACTTCTGCTGTTTCACTCGGTGATGTTCTGTTGC 781
Db 361 GAGGAAGCAGTCATTTTGAATTTTCACTTCTGCTGTTTCACTCGGTGATGTTCTGTTGC 420
Qy 782 TGTTTCTTATCATTTGCGGATGTTAGGATTTGCGAAGCGGTGAAGAAATCTGTTG 841
Db 421 TGTTTCTTATCATTTGCGGATGTTAGGATTTGCGAAGCGGTGAAGAAATCTGTTG 480
Qy 842 CTTCCTGATGATGTTTGGAGTTTGTCTGTTCACTTTTCTGTAGAACTGGCTTGTGC 901
Db 481 CTTCCTGATGATGTTTGGAGTTTGTCTGTTCACTTTTCTGTAGAACTGGCTTGTGC 540
Qy 902 GTTTGGAATATGAACAGAACTTATGTTTCCAGTACAAATGTCAGATATGGTCACTTTG 961
Db 541 GTTTGGAATATGAACAGAACTTATGTTTCCAGTACAAATGTCAGATATGGTCACTTTG 600
Qy 962 AAAGCCAGGATGACAAATTTAGGATTTACCTAGATATCGTGGCTTACCTCATGCTTGAAT 1021
Db 601 AAAGCCAGGATGACAAATTTAGGATTTACCTAGATATCGTGGCTTACCTCATGCTTGAAT 660
Qy 1022 TTTTTCAGAGAGTAAAGTGTGAGTATATTTTCACTGATGTTGTTGAAATG 1081
Db 661 TTTTTCAGAGAGTAAAGTGTGAGTATATTTTCACTGATGTTGTTGAAATG 720
Qy 1082 ACAGAGATGAGTGGCGCCCGAGTTCTGCTGTGTTAGAGATTTCCAGAGTGTTCCTCAA 1141
Db 721 ACAGAGATGAGTGGCGCCCGAGTTCTGCTGTGTTAGAGATTTCCAGAGTGTTCCTCAA 780
Qy 1142 CAGGCGCCAGGAGATCTCAGTCACTTTTATCAAGAGGTTGTGGGAAGAAATGTAT 1201
Db 781 CAGGCGCCAGGAGATCTCAGTCACTTTTATCAAGAGGTTGTGGGAAGAAATGTAT 840
Qy 1202 TCCTTTTTCAGAGAGAACCAACACTGAGTGTGAGTGTTCGGGATCTCCATTTGG 1261
Db 841 TCCTTTTTCAGAGAGAACCAACACTGAGTGTGAGTGTTCGGGATCTCCATTTGG 900
Qy 1262 GTGACACAAATCCTCGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db 901 GTGACACAAATCCTCGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy 1322 AGAAGGAGCGCGGAGACAGACAAATGATGCTTTGAAAGATGACAACTCTCAGCACCTG 1381
Db 961 AGAAGGAGCGCGGAGACAGACAAATGATGCTTTGAAAGATGACAACTCTCAGCACCTG 1020
Qy 1382 TCATCTCCCTCAGTAGAAGTGTGAAACCAAGCGCTGTCAAGAACTTTTGAACACACATCC 1441
Db 1021 TCATCTCCCTCAGTAGAAGTGTGAAACCAAGCGCTGTCAAGAACTTTTGAACACACATCC 1080
Qy 1442 ATGGCAAAACAGCTTTTAAATACACACTTTGAGATGAGGAGTATAAAAAGAAATGTACAG 1501
Db 1081 ATGGCAAAACAGCTTTTAAATACACACTTTGAGATGAGGAGTATAAAAAGAAATGTACAG 1140
Qy 1502 AAGAAAAACAAACTTGTGTTTACGAGTGTGAAATTTTGGTACATACATCTGTTT 1561
Db 1141 AAGAAAAACAAACTTGTGTTTATTTGAGTGTGAAATTTTGGTACATACATCTGTTT 1200
Qy 1562 CAGAAATATGTAGAAATAAATAATGTTGCCATAAATAAACACCTAAGCATATACTATTCTA 1621

Db 1201 CAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACACCTAAGCATATACATATCTTA 1260
Qy 1622 TGCTTTAAATAGAGATGGAAGATTTTCATGTCTAAGTCACACCTGGACCAATATTTGA 1681
Db 1261 TGCTTTAAATAGAGATGGAAGATTTTCATGTCTAAGTCACACCTGGACCAATATTTGA 1320
Qy 1682 TGCCCTTAAATGCTGAAGACAGATGTCAACCACCTGTGTAGCCCTGTGTATGACTTTTA 1741
Db 1321 TGCCCTTAAATGCTGAAGACAGATGTCAACCACCTGTGTAGCCCTGTGTATGACTTTTA 1380
Qy 1742 CTGAACACAGTATGTTTTCAGGACGAGCATGTTTGTATGATTTCCGGATCCATCAAA 1801
Db 1381 CTGAACACAGTATGTTTTCAGGACGAGCATGTTTGTATGATTTCCGGATCCATCAAA 1440
Qy 1802 CGAGTCACATATGTTGGGACTGGAGCATAGTAAAGTTGATTTACTTCTCAACACTAGT 1861
Db 1441 CGAGTCACATATGTTGGGACTGGAGCATAGTAAAGTTGATTTACTTCTCAACACTAGT 1500
Qy 1862 ATATAAGTACTAATTAATGCTTAACATAGGAAGTTAGAAATACATAAATCTTTATTA 1921
Db 1501 ATATAAGTACTAATTAATGCTTAACATAGGAAGTTAGAAATACATAAATCTTTATTA 1560
Qy 1922 CTCAGGATCTATTTCTGATCTAAATAAATATATATATATATATATATATATATATAT 1981
Db 1561 CTCAGGATCTATTTCTGATCTAAATAAATATATATATATATATATATATATATATAT 1620
Qy 1982 TGACTACCTAAATGTGATTTTCTGCTTACTTAATAATATCTTACCATTAAAGCAAA 2041
Db 1621 TGACTACCTAAATGTGATTTTCTGCTTACTTAATAATATCTTACCATTAAAGCAAA 1680
Qy 2042 GCTAACACATGCTTAAGCTGATCAGGATTTTGTATATAAGTCCTGTAAATCTG 2101
Db 1681 GCTAACACATGCTTAAGCTGATCAGGATTTTGTATATAAGTCCTGTAAATCTG 1740
Qy 2102 TATAATTCAGTCGATTTTCAGTCTGATTAAGTTAAGAAATACCATTTAGAAAGCAAA 2161
Db 1741 TATAATTCAGTCGATTTTCAGTCTGATTAAGTTAAGAAATACCATTTAGAAAGCAAA 1800
Qy 2162 TTGTCCTGTATAGCATCATTTATTTAGCCTTTCCGTTTAAATAAGCTTTACTTCTGT 2221
Db 1801 TTGTCCTGTATAGCATCATTTATTTAGCCTTTCCGTTTAAATAAGCTTTACTTCTGT 1860
Qy 2222 CCTGGCTTATATTACACATATACTGTTATTTAAATACCTTAAACCACTAAATTTGAAAT 2281
Db 1861 CCTGGCTTATATTACACATATACTGTTATTTAAATACCTTAAACCACTAAATTTGAAAT 1920
Qy 2282 TACCAGTGTATACATAGGAATCATTTATTCAGNATGTCTGGCTTTTAGAGATTTA 2341
Db 1921 TACCAGTGTATACATAGGAATCATTTATTCAGNATGTCTGGCTTTTAGAGATTTA 1980
Qy 2342 ATAAGAAATTTGCACATACCTTAGTGTGATTCAGAAAGGACTGTATGCTGTTTCTCC 2401
Db 1981 ATAAGAAATTTGCACATACCTTAGTGTGATTCAGAAAGGACTGTATGCTGTTTCTCC 2040
Qy 2402 CAAATGAAGCTCTTTTGACACTAAACACTTTTTHAAAAGCTTATCTTTGGCTTCTCA 2461
Db 2041 CAAATGAAGCTCTTTTGACACTAAACACTTTTTHAAAAGCTTATCTTTGGCTTCTCA 2100
Qy 2462 AACAGAAAGCAATAGTCTCCAGTCAATATAAATCTACAGAAATAGTGTCTTTTCT 2521
Db 2101 AACAGAAAGCAATAGTCTCCAGTCAATATAAATCTACAGAAATAGTGTCTTTTCT 2160
Qy 2522 CAGAAAAATGCTTGTAGAAATCATTTAAACATGTGACAAATTTAGAGATTTCTTTGTTTA 2581
Db 2161 CCAGAAAAATGCTTGTAGAAATCATTTAAACATGTGACAAATTTAGAGATTTCTTTGTTTA 2220
Qy 2582 TTTCACTGATTAATATACGTGCAAAATTTACACAGATTTAATAATTTTTCACAGAGTA 2641
Db 2221 TTTCACTGATTAATATACGTGCAAAATTTACACAGATTTAATAATTTTTCACAGAGTA 2280
Qy 2642 TAGTATATTATTTGAAATGGGAAAGTCATTTTACTGATTTTGTGATTTTCTTTAT 2701

Db 2281 TAGTATATTATTTGAAATGGGAAAGTCATTTTACTGTATTTTGTATTTTGTAT 2340
Qy 2702 TTCTCAGATATGGAAGAAATTTAAATATGTGTCAATAAATATTTTCTAGAGATAA 2758
Db 2341 TTCTCAGATATGGAAGAAATTTAAATATGTGTCAATAAATATTTTCTAGAGATAA 2397

RESULT 5
US-10-201-858-323
; Sequence 323, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 AGAGAAAGAGCGTCTCCAGCTGAAGCCAATCAGAGCCCTCCGCTCTCCGCGAAGATT 421
Db 1 AGAGAAAGAGCGTCTCCAGCTGAAGCCAATCAGAGCCCTCCGCTCTCCGCGAAGATT 60
Qy 422 CCTTCCCCCATGAGCCCCCGCGTCCCGACTATCCCGAGCGGCGGTGGGCGAC 481
Db 61 CCTTCCCCCATGAGCCCCCGCGTCCCGACTATCCCGAGCGGCGGTGGGCGAC 120
Qy 482 CGGCCCCAGCGCGAGCATCGCTGCTTTTGGCTTTGGAGTAGGATGTGTGAAGGA 541
Db 121 CGGCCCCAGCGCGAGCATCGCTGCTTTTGGCTTTGGAGTAGGATGTGTGAAGGA 180
Qy 542 TGGGGCTTCTCCCTTAGCGGGCTCACAAATGGCCAGAGAGATTCCGTGAAGATGCTCTCGC 601

181 TGCGGCTTCCCTTACGGGCTCACAAATGGCCAGAGAGATTCCTGTAAGTGTCTGGCC 240
602 TGCTGTCTACGCCCTCAATCTGCTCTTTTGGTAAATGTCATCAGTGTGTGGCAGTT 661
241 TGCTGTCTACGCCCTCAATCTGCTCTTTTGGTAAATGTCATCAGTGTGTGGCAGTT 300
662 TCTGCTTGGATGAGGAGTACCTAAATATGTTCTCACTTTAACTGCAAGAACGAGGTA 721
301 TCTGCTTGGATGAGGAGTACCTAAATATGTTCTCACTTTAACTGCAAGAACGAGGTA 360
722 GAGGAGCAGTCACTTTGAGGAGTACCTTTCCGTGGTTCATCCGGTCATGATGCTGTTGC 781
361 GAGGAGCAGTCACTTTGAGGAGTACCTTTCCGTGGTTCATCCGGTCATGATGCTGTTGC 420
782 TGTTCCTTATCATTTGCGGAGTGTAGGATATGTTGGAACCGTGAAGAAATCTGTTG 841
421 TGTTCCTTATCATTTGCGGAGTGTAGGATATGTTGGAACCGTGAAGAAATCTGTTG 480
842 CTTCTTCGATGTTGAGGAGTGTAGGATATGTTGGAACCGTGAAGAAATCTGTTG 901
481 CTTCTTCGATGTTGAGGAGTGTAGGATATGTTGGAACCGTGAAGAAATCTGTTG 540
902 GTTTGGACATGAAACAGGAACTTATGTTCCAGTACAATGCTCAGATATGTTGCTTTG 961
541 GTTTGGACATGAAACAGGAACTTATGTTCCAGTACAATGCTCAGATATGTTGCTTTG 600
962 AAAGCCAGGATGACAAATATGGAATACCTAGATATGCGTGGCTTACTATGCTTGGAT 1021
601 AAAGCCAGGATGACAAATATGGAATACCTAGATATGCGTGGCTTACTATGCTTGGAT 660
1022 TTTTTCCTCAGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1081
661 TTTTTCCTCAGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 720
1082 ACAGAGATGAGTGGCCGCCAGATTCCTGCTGTGTAGAGAAATCCAGAGATGTTCCAA 1141
721 ACAGAGATGAGTGGCCGCCAGATTCCTGCTGTGTAGAGAAATCCAGAGATGTTCCAA 780
1142 CAGGCCACAGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1201
781 CAGGCCACAGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 840
1202 TCCCTTTTGGAGAGAAACCAACAACTGCGTGTGTAGGAGTGTAGGAGTGTAGGAGT 1261
841 TCCCTTTTGGAGAGAAACCAACAACTGCGTGTGTAGGAGTGTAGGAGTGTAGGAGT 900
1262 GTGACAAATCTGGCCATGATCTCAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
901 GTGACAAATCTGGCCATGATCTCAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
1322 AGRAGGAGCGGGGAGAGACCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG 1381
961 AGRAGGAGCGGGGAGAGACCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG 1020
1382 TCATGTCCTCAGTAGAATCTGTTGAACCAAGCCTGTCAAGAAATCTTGAACACACATCC 1441
1021 TCATGTCCTCAGTAGAATCTGTTGAACCAAGCCTGTCAAGAAATCTTGAACACACATCC 1080
1442 ATGCAAAACAGCTTTATACACCTTTGAGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1501
1081 ATGCAAAACAGCTTTATACACCTTTGAGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1140
1502 AGRAGGAGCGGGGAGAGACCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG 1561
1141 AGRAGGAGCGGGGAGAGACCAATGATGTCCTTGAAGATGACAACTCTCAGACCTG 1200
1562 CAGAAATATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1621
1201 CAGAAATATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1260
1622 TGTCTTAAATGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1681

1261 TGTCTTAAATGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1320
1682 TGCCCTTAAATGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1741
1321 TGCCCTTAAATGAGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1380
1742 CTGAACACAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1801
1381 CTGAACACAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1440
1802 CGAGTCACATATGTTGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1861
1441 CGAGTCACATATGTTGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1500
1862 ATATAAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1921
1501 ATATAAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1560
1922 CTCAGGATGTATCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1981
1561 CTCAGGATGTATCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1620
1982 TGACTACCTAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2041
1621 TGACTACCTAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1680
2042 GCTACACATGCTCTTAAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2101
1681 GCTACACATGCTCTTAAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1740
2102 TATAATTCAGTGTGATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2161
1741 TATAATTCAGTGTGATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1800
2162 TTGCTGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2221
1801 TTGCTGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1860
2222 CTTGGCTTATATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2281
1861 CTTGGCTTATATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
2282 TACAGTGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2341
1921 TACAGTGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 1980
2342 ATAAGAAATTTGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2401
1981 ATAAGAAATTTGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
2402 CAATGAGACCTCTTTTGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2461
2041 CAATGAGACCTCTTTTGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2100
2462 AACAGAGCAATGCTCCAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2521
2101 AACAGAGCAATGCTCCAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2160
2522 CCAGAAATTTGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2581
2161 CCAGAAATTTGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2220
2582 TTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2641
2221 TTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
2642 TAGTATATTTTGAATGAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2701
2281 TAGTATATTTTGAATGAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2340
2702 TTTCTAGATGAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2758
2341 TTTCTAGATGAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGTGTAGGAGT 2397

RESULT 6

US-10-205-890-323
; Sequence 323, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P34301C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-205-890-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	DB	362	AGAGAAAGAGCTCTCCAGCTGAAGCCCAATGAGCCCTCCGGCTCTCCGCGAAGAGTT	421
DB		1	AGAGAAAGAGCGCTCTCCAGCTGAAGCCCAATGAGCCCTCCGGCTCTCCGCGAAGAGTT	60
QY		422	CCCTGCCCGGATGAGCCCGCGCTCGTCCCGACTATCCCGAGCGGGCGTGGGGAC	481
DB		61	CCCTGCCCGGATGAGCCCGCGCTCGTCCCGACTATCCCGAGCGGGCGTGGGGAC	120
QY		482	CGGGCCGAGCGCGAGATCGTCCGCTTTTGGCCCTTGGAGTAGAGTGTGTGAAGA	541
DB		121	CGGGCCGAGCGCGAGATCGTCCGCTTTTGGCCCTTGGAGTAGAGTGTGTGAAGA	180
QY		542	TGGGGCTTCTCCCTTACGGGGCTCAATGGCCGAGAGAGATCCGTGAAGTGTCTGGC	601
DB		181	TGGGGCTTCTCCCTTACGGGGCTCAATGGCCGAGAGAGATCCGTGAAGTGTCTGGC	240
QY		602	TGCCTGCTTACGCCCTCAATCTGCTTTTGGTTAATCTCCATCAGTGTGTGGCAGTT	661

DB	241	TGCTGCTCTAGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTT	300
QY	662	TCTGCTTGGATGAGGACTACCTAAATAATTTCTCACTTTTAACTCAGAAACGAGGTA	721
DB	301	TCTGCTTGGATGAGGACTACCTAAATAATTTCTCACTTTTAACTCAGAAACGAGGTA	360
QY	722	GAGGAGCAGTCATTTGACCTTACTTTCTCTGCTGCTCATCGGTCATGATGCTGTTGC	781
DB	361	GAGGAGCAGTCATTTGACCTTACTTTCTCTGCTGCTCATCGGTCATGATGCTGTTGC	420
QY	782	TGTTTCTTATCATTTGCGGAGTGTAGGATATTGTGGAAACCGTCAAAAGAAATCTCTTG	841
DB	421	TGTTTCTTATCATTTGCGGAGTGTAGGATATTGTGGAAACCGTCAAAAGAAATCTCTTG	480
QY	842	CTTCTTGATGCTTCTTTGGAAGTTTCTGCTCAATTTTCTGTGTAGAACTGGCTTGTGC	901
DB	481	CTTCTTGATGCTTCTTTGGAAGTTTCTGCTCAATTTTCTGTGTAGAACTGGCTTGTGC	540
QY	902	GTTTGGACATATGAACAGAACTTATGTTCCAGTACAAATGCTCAGATATGCTCACTTTG	961
DB	541	GTTTGGACATATGAACAGAACTTATGTTCCAGTACAAATGCTCAGATATGCTCACTTTG	600
QY	962	AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGTTGGAAT	1021
DB	601	AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGTTGGAAT	660
QY	1022	TTTTTTTCCAGAGAGTTTAAAGTCTGCTGGAGTAGTATATTCATGCTGCTGGTGAATG	1081
DB	661	TTTTTTTCCAGAGAGTTTAAAGTCTGCTGGAGTAGTATATTCATGCTGCTGGTGAATG	720
QY	1082	ACAGAGATGAGTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCAGAGATGTTCCAAA	1141
DB	721	ACAGAGATGAGTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCAGAGATGTTCCAAA	780
QY	1142	CAGGCCACAGGAGATCTCAGTGACCTTTATCAAGAGGTTGTGGAGAGAAATGATAT	1201
DB	781	CAGGCCACAGGAGATCTCAGTGACCTTTATCAAGAGGTTGTGGAGAGAAATGATAT	840
QY	1202	TCTTTTGTAGAGGAAACCAAACTCAGTGCTGTGAGTTTCTGGAAATCTCCATGGG	1261
DB	841	TCTTTTGTAGAGGAAACCAAACTCAGTGCTGTGAGTTTCTGGAAATCTCCATGGG	900
QY	1262	GTGACAAATCTTGGCCATGATTTCTCACCATTACTCTGCTGCTGGGCTGTGATATGAT	1321
DB	901	GTGACAAATCTTGGCCATGATTTCTCACCATTACTCTGCTGCTGGGCTGTGATATGAT	960
QY	1322	AGAGGGAGCGGGGACAGACCAATGATGTCCTTGAAGAAATGACAACTCTCAGCACCTG	1381
DB	961	AGAGGGAGCGGGGACAGACCAATGATGTCCTTGAAGAAATGACAACTCTCAGCACCTG	1020
QY	1382	TCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAAATCTTTGAACACATCC	1441
DB	1021	TCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAAATCTTTGAACACATCC	1080
QY	1442	ATGCAACAGCTTTATACACACTTTGAGATGAGAGTTTAAAGAAATGTCACAG	1501
DB	1081	ATGCAACAGCTTTTAAATACACACTTTGAGATGAGAGTTTAAAGAAATGTCACAG	1140
QY	1502	AAGAAACCAAACTTTTACTGGACTTGTGAATTTTGTAGTACATACATGTTGTTT	1561
DB	1141	AAGAAACCAAACTTTTACTGGACTTGTGAATTTTGTAGTACATACATGTTGTTT	1200
QY	1562	CAGAAATATGTAGAAATAAAATGTTGCCATAAAATACACCTTGAAGATATCTATCTA	1621
DB	1201	CAGAAATATGTAGAAATAAAATGTTGCCATAAAATACACCTTGAAGATATCTATCTA	1260
QY	1622	TGCTTTAAATGAGGATGGAAGAGTTTCAATGTCATAGTCAACCTTGAACATAATTA	1681
DB	1261	TGCTTTAAATGAGGATGGAAGAGTTTCAATGTCATAGTCAACCTTGAACATAATTA	1320
QY	1682	TGCGCTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTGATGCTTTTA	1741
DB	1321	TGCGCTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTGATGCTTTTA	1380

QY 1742 CTGAACACAGTATGTTTGGAGCAGCATGGTTGATTAGCATTTCCGCATCCATGCAA 1801
Db 1381 CTGAACACAGTATGTTTGGAGCAGCATGGTTGATTAGCATTTCCGCATCCATGCAA 1440
QY 1802 CGAGTCACATATGCTGGAGCTGGAGCATAGTAAAGGTTGATTACTTCTACCAACTAGT 1861
Db 1441 CGAGTCACATATGCTGGAGCTGGAGCATAGTAAAGGTTGATTACTTCTACCAACTAGT 1500
QY 1862 ATATAAGTACTAATTAATGCTAAACATAGGAAGTAGAATAAATACATAAATCTTTATTA 1921
Db 1501 ATATAAGTACTAATTAATGCTAAACATAGGAAGTAGAATAAATACATAAATCTTTATTA 1560
QY 1922 CTGAGGATCTATCTCTGATGCTAAATAATATATATATATATATATATATATATATG 1981
Db 1561 CTGAGGATCTATCTCTGATGCTAAATAATATATATATATATATATATATATATATG 1620
QY 1982 TGACTACCTAAATGCTGTTTGGCTGTTACTAAATATATCTTACCACTTAAAGAGCAA 2041
Db 1621 TGACTACCTAAATGCTGTTTGGCTGTTACTAAATATATCTTACCACTTAAAGAGCAA 1680
QY 2042 GCTAAACATCTGCTTAAGCTGATCAGGATTTTGGTATATATATATATATATATATG 2101
Db 1681 GCTAAACATCTGCTTAAGCTGATCAGGATTTTGGTATATATATATATATATATATG 1740
QY 2102 TATAATTCAGTCGATTTTCTGATATATGTTAAGAATAACCATATGAAAAGGAAAT 2161
Db 1741 TATAATTCAGTCGATTTTCTGATATATGTTAAGAATAACCATATGAAAAGGAAAT 1800
QY 2162 TTGCTGTTAGATCATATTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTCTCT 2221
Db 1801 TTGCTGTTAGATCATATTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTCTGT 1860
QY 2222 CCTGGGCTTATATACATATACTGTTTAAATATATATATATATATATATATATATATAT 2281
Db 1861 CCTGGGCTTATATACATATACTGTTTAAATATATATATATATATATATATATATAT 1920
QY 2282 TACAGTGTGATACATAGGAATCATATTCAGAAATGATGCTGCTTGGCTTGGAGTATTA 2341
Db 1921 TACAGTGTGATACATAGGAATCATATTCAGAAATGATGCTGCTTGGCTTGGAGTATTA 1980
QY 2342 ATAGAAATTTGCATATCTAGTTGATTCAGAAAGGCTTGTATGCTGTTTCTCTCC 2401
Db 1981 ATAGAAATTTGCATATCTAGTTGATTCAGAAAGGCTTGTATGCTGTTTCTCTCC 2040
QY 2402 CAATGAAGACTCTTTTGGACATTAACACTTTTAAAGGCTTATCTTGGCTTCTCCA 2461
Db 2041 CAATGAAGACTCTTTTGGACATTAACACTTTTAAAGGCTTATCTTGGCTTCTCCA 2100
QY 2462 AACAGAGCAATAGTCTCAAGTCAATATAAATCTACAGAAATAGTCTTCTTTCT 2521
Db 2101 AACAGAGCAATAGTCTCAAGTCAATATAAATCTACAGAAATAGTCTTCTTTCT 2160
QY 2522 CCAGAAATGCTTGTGAGATCATTAATAACATGTCAGAAATTTAGAGATTTCTTTGTTTA 2581
Db 2161 CCAGAAATGCTTGTGAGATCATTAATAACATGTCAGAAATTTAGAGATTTCTTTGTTTA 2220
QY 2582 TTTCACTGATTAATATATCTGTCGCAATATACAGATTTATTAATTTTACAGAGTA 2641
Db 2221 TTTCACTGATTAATATATCTGTCGCAATATACAGATTTATTAATTTTACAGAGTA 2280
QY 2642 TAGTATATTTTGAATGGAAGTGAATTTTACTGATTTTGTGTTTGTATTTGTTAT 2701
Db 2281 TAGTATATTTTGAATGGAAGTGAATTTTACTGATTTTGTGTTTGTATTTGTTAT 2340
QY 2702 TTCTCAGAAATGGAAGAAATTTAAATATGTCATATAATTTTCTAGAGTAA 2758
Db 2341 TTCTCAGAAATGGAAGAAATTTAAATATGTCATATAATTTTCTAGAGTAA 2397

RESULT 7
US-10-208-024-323
; Sequence 323, Application US/10208024

/ Publication No. US20040048335A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P34301C538
/ CURRENT APPLICATION NUMBER: US/10/208,024
/ CURRENT FILING DATE: 2002-07-29
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 323
/ LENGTH: 2397
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-208-024-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 362 ACAGAAAGAGCGCTCCAGCTGAGCCCAATGACGCTCCGGCTCTCCGGAGAGGTT 421
Db -1 ACAGAAAGAGCGCTCCAGCTGAGCCCAATGACGCTCCGGCTCTCCGGAGAGGTT 60
QY 422 CCTCTCCCGATGAGCCCCCGCGCTGCGTCCCGACTATCCCGCGGGGTGGGGCAC 481
Db .61 CCTCTCCCGATGAGCCCCCGCGCTGCGTCCCGACTATCCCGCGGGGTGGGGCAC 120
QY 482 CCGGCCCCAGCGCGAGATCGCTGCGCTTTTCCCTTGGAGTAGGATGCTGTAAGGA 541
Db 121 CCGGCCCCAGCGCGAGATCGCTGCGCTTTTCCCTTGGAGTAGGATGCTGTAAGGA 180
QY 542 TGGGGCTTCTCCCTTACGGGGCTCAATGGCCAGAGAGATTCGGTGAAGTGTCTGCGC 601
Db 181 TGGGGCTTCTCCCTTACGGGGCTCAATGGCCAGAGAGATTCGGTGAAGTGTCTGCGC 240
QY 602 TGCCTGCTCTAGCGCTCAATCTGCTTTTGGTTAATGTCATCAGTGTGTGTCAGTT 661
Db 241 TGCCTGCTCTAGCGCTCAATCTGCTTTTGGTTAATGTCATCAGTGTGTGTCAGTT 300
QY 662 TCTGCTTGGATGAGGACTTACCTAATAATATGTTCTACCTTTTAACTGCAGAAACGAGGTA 721
Db 301 TCTGCTTGGATGAGGACTTACCTAATAATATGTTCTACCTTTTAACTGCAGAAACGAGGTA 360

722 GAGGAGCAGTCATTTTGGCTTACTTCTCTGTTGGTTTCATCCGGTCATGTTCTGTTTGC 781
Db
361 GAGGAGCAGTCATTTTGGCTTACTTCTCTGTTGGTTTCATCCGGTCATGTTCTGTTTGC 420
Qy
782 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGGAAACGGTGAAGAAATCTGTTG 841
Db
421 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGGAAACGGTGAAGAAATCTGTTG 480
Qy
842 CTCTTTCATGTTTGGGATGTTAGGATATTTGGGAAACGGTGAAGAAATCTGTTG 901
Db
481 CTCTTTCATGTTTGGGATGTTAGGATATTTGGGAAACGGTGAAGAAATCTGTTG 540
Qy
902 GTTTTGGACATATGAACAGGAACTTATGTTTCCAGTACAATGGTCAGATATGGTCACCTTG 961
Db
541 GTTTTGGACATATGAACAGGAACTTATGTTTCCAGTACAATGGTCAGATATGGTCACCTTG 600
Qy
962 AAAGCCAGGATGACAAATATGATTTACCTAGATATCGGTGGCTTACTCATGCTTGGAA 1021
Db
601 AAAGCCAGGATGACAAATATGATTTACCTAGATATCGGTGGCTTACTCATGCTTGGAA 660
Qy
1022 TTTTTCCTCAGAGAGGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACCTGGTTGGAAATG 1081
Db
661 TTTTTCCTCAGAGAGGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACCTGGTTGGAAATG 720
Qy
1082 ACAGAGATGAGTGGCCCCAGATTCCTGCTGTGTAGAGAAATCCAGATGTTCCAAA 1141
Db
721 ACAGAGATGAGTGGCCCCAGATTCCTGCTGTGTAGAGAAATCCAGATGTTCCAAA 780
Qy
1142 CAGGCCACAGAGAGATCTCAGTGACCTTTATCAGAGAGGTTGTGGGAGAAATGAT 1201
Db
781 CAGGCCACAGAGAGATCTCAGTGACCTTTATCAGAGAGGTTGTGGGAGAAATGAT 840
Qy
1202 TCCTTTTGGAGAGAACCAACAACTGCAGTGCTGTGGGATTCCTCCATTTGGG 1261
Db
841 TCCTTTTGGAGAGAACCAACAACTGCAGTGCTGTGGGATTCCTCCATTTGGG 900
Qy
1262 GTGACAAATCTGGCCATGATTTCAACATTTACTCTGCTGGGCTCTGATTTGAT 1321
Db
901 GTGACAAATCTGGCCATGATTTCAACATTTACTCTGCTGGGCTCTGATTTGAT 960
Qy
1322 AGAAGGAGCGGGGAGACCAAAATGATGCTCTGAAGAAATGACAACTCTCAGACCTG 1381
Db
961 AGAAGGAGCGGGGAGACCAAAATGATGCTCTGAAGAAATGACAACTCTCAGACCTG 1020
Qy
1382 TCATGTCCTCTGATAGAACTGTTGAAACCAAGCTCTCAAGATCTTTGAACACATCC 1441
Db
1021 TCATGTCCTCTGATAGAACTGTTGAAACCAAGCTCTCAAGATCTTTGAACACATCC 1080
Qy
1442 ATGCAAAACAGCTTTAATACACACTTTGAGATGGAGGTTTAAAGAAATGTCACAG 1501
Db
1081 ATGCAAAACAGCTTTAATACACACTTTGAGATGGAGGTTTAAAGAAATGTCACAG 1140
Qy
1502 AGAAGAACCAAACTGTTTACTGACCTGTGAATTTTGAATCATPACTATGTTT 1561
Db
1141 AGAAGAACCAAACTGTTTACTGACCTGTGAATTTTGAATCATPACTATGTTT 1200
Qy
1562 CAGAAATATGAAATATAATGTTGCCATATAATATAACCTTAGCATATCTATCTTA 1621
Db
1201 CAGAAATATGAAATATAATGTTGCCATATAATATAACCTTAGCATATCTATCTTA 1260
Qy
1622 TGCTTTAAATAGGATGAAAGTTTCTATGTCATAGTCAACACCTGGACCAATATGA 1681
Db
1261 TGCTTTAAATAGGATGAAAGTTTCTATGTCATAGTCAACACCTGGACCAATATGA 1320
Qy
1682 TGCCCTTAAATGCTGAAGACAGATGTCATACCCTGTGTAGCTGTGTATGACTTTTA 1741
Db
1321 TGCCCTTAAATGCTGAAGACAGATGTCATACCCTGTGTAGCTGTGTATGACTTTTA 1380
Qy
1742 CTGAACACAGTTATGTTTTCAGGACAGCTGTTTGAATAGCTTCCGATCCATGCCAA 1801
Db
1381 CTGAACACAGTTATGTTTTCAGGACAGCTGTTTGAATAGCTTCCGATCCATGCCAA 1440

1802 CGAGTCACATATGTTGGGACTGGAGCCATAGTAAAGTTGATTTTACTTCTACCAACTAGT 1861
Db
1441 CGAGTCACATATGTTGGGACTGGAGCCATAGTAAAGTTGATTTTACTTCTACCAACTAGT 1500
Qy
1862 ATATAAGTACTATAATTAATGCTAACATAGGAGTTTGAAGAAATCTAATACTTTTATTA 1921
Db
1501 ATATAAGTACTATAATTAATGCTAACATAGGAGTTTGAAGAAATCTAATACTTTTATTA 1560
Qy
1922 CTCACGATCTATTTCTCTGATGCTAAATAATATATATATATATATATATATATATAT 1981
Db
1561 CTCACGATCTATTTCTCTGATGCTAAATAATATATATATATATATATATATATATATAT 1620
Qy
1982 TGACTACCTAAATGATTTTGTGGTCTACTAAATATTTCTTACCACCTTAAAGAGCAA 2041
Db
1621 TGACTACCTAAATGATTTTGTGGTCTACTAAATATTTCTTACCACCTTAAAGAGCAA 1680
Qy
2042 GCTAACACATTTCTTAAGCTGATCAGGATTTTGTATATATATATATATATATATATATAT 2101
Db
1681 GCTAACACATTTCTTAAGCTGATCAGGATTTTGTATATATATATATATATATATATATAT 1740
Qy
2102 TATAATTCAGTCGATTTTCAGTTCTGATAATGTTTAAAGAAATACCAATATGAAAGGAAAT 2161
Db
1741 TATAATTCAGTCGATTTTCAGTTCTGATAATGTTTAAAGAAATACCAATATGAAAGGAAAT 1800
Qy
2162 TTGCTCTGTATAGCATCATTTATTTTGTAGCTTCTCTGTTAAAGAAATTTTCTTCTGT 2221
Db
1801 TTGCTCTGTATAGCATCATTTATTTTGTAGCTTCTCTGTTAAAGAAATTTTCTTCTGT 1860
Qy
2222 CTTGGCTTTATTTTACATATAACTGTTTAAATTAATTTTAACTTAACTTAACTTAACTTAA 2281
Db
1861 CTTGGCTTTATTTTACATATAACTGTTTAAATTAATTTTAACTTAACTTAACTTAACTTAA 1920
Qy
2282 TACCAGTGTGATACATAGGAATCATTTTCAAGATGATGCTGCTTTTAAAGAAATTTA 2341
Db
1921 TACCAGTGTGATACATAGGAATCATTTTCAAGATGATGCTGCTTTTAAAGAAATTTA 1980
Qy
2342 ATAGAAATTTTGCACATTAATTTTGTAGTTTGAAGAGGCTGATGCTGTTTCTCTCC 2401
Db
1981 ATAGAAATTTTGCACATTAATTTTGTAGTTTGAAGAGGCTGATGCTGTTTCTCTCC 2040
Qy
2402 CAAATGAAGACTCTTTTGTGACATTAACACTTTTAAAGAAATTTTAAAGCTTTCTTCCA 2461
Db
2041 CAAATGAAGACTCTTTTGTGACATTAACACTTTTAAAGAAATTTTAAAGCTTTCTTCCA 2100
Qy
2462 AACAGAGCAATGATCTCCAGTCAATATAATTTTCAAGAAATAGTGTCTTTTCT 2521
Db
2101 AACAGAGCAATGATCTCCAGTCAATATAATTTTCAAGAAATAGTGTCTTTTCT 2160
Qy
2522 CCAGAAATTTTGTGACATTAATTTTGTAGTTTGAAGAGGCTGATGCTGTTTCTCTCC 2581
Db
2161 CCAGAAATTTTGTGACATTAATTTTGTAGTTTGAAGAGGCTGATGCTGTTTCTCTCC 2220
Qy
2582 TTTCACTGATTAATATATCTGTGGCAATTTACAGATTTATTAATTTTAAAGAAATTTTCAAGAGTA 2641
Db
2221 TTTCACTGATTAATATATCTGTGGCAATTTACAGATTTATTAATTTTAAAGAAATTTTCAAGAGTA 2280
Qy
2642 TAGTATATTTTGAATGGAAGGCTGATTTTCTGATTTTGTGATTTTGTGTTTAT 2701
Db
2281 TAGTATATTTTGAATGGAAGGCTGATTTTCTGATTTTGTGATTTTGTGTTTAT 2340
Qy
2702 TTCTCAGATATGGAAGAAATTTTAAATGCTGCAATAATTTTCTAGAGAGTAA 2758
Db
2341 TTCTCAGATATGGAAGAAATTTTAAATGCTGCAATAATTTTCTAGAGAGTAA 2397

RESULT 8

US-101-853-323
; Sequence 323, Application US/10201853
; Publication No. US2004005358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey	Qy	782	TGTTTCCTTATCATTTGGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTG	841
APPLICANT: Godowski, Paul J.	Db	421	TGTTTCCTTATCATTTGGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTG	480
APPLICANT: Gurney, Austin L.	Qy	842	CTTCTTGATGTGATCTTTGGAAAGTTTGGTGTGTCATTTTCTGTGTAGAACTGGCTTGGC	901
APPLICANT: Pan, James	Db	481	CTTCTTGATGTGATCTTTGGAAAGTTTGGTGTGTCATTTTCTGTGTAGAACTGGCTTGGC	540
APPLICANT: Smith, Victoria	Qy	902	GTTTGGACATATGAACAGGAACCTTATGGTTCAGTACAAATGCTCAGATATGCTCACTTTG	961
APPLICANT: Watanabe, Colin K.	Db	541	GTTTGGACATATGAACAGGAACCTTATGGTTCAGTACAAATGCTCAGATATGCTCACTTTG	600
APPLICANT: Wood, William I.	Qy	962	AAAGCCAGGATGACAAATATGATGATACCTAGATATCGGTGGCTTACTCATCTTGGAT	1021
APPLICANT: Zhang, Zemin	Db	601	AAAGCCAGGATGACAAATATGATGATACCTAGATATCGGTGGCTTACTCATCTTGGAT	660
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	Qy	1022	TTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTGTGAAATG	1081
TITLE OF INVENTION: ACIDS ENCODING THE SAME	Db	661	TTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTGTGAAATG	720
FILE REFERENCE: P3430R1C465	Qy	1082	ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCAGGATGTTCCAAA	1141
CURRENT APPLICATION NUMBER: US/10/201.853	Db	721	ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCAGGATGTTCCAAA	780
PRIOR FILING DATE: 2002-07-23	Qy	1142	CAGGCCACAGGAGATCTCAGTACCTTTATCAAGAGGTTGTGGGAAGAAATGAT	1201
PRIOR APPLICATION NUMBER: 10/052586	Db	781	CAGGCCACAGGAGATCTCAGTACCTTTATCAAGAGGTTGTGGGAAGAAATGAT	840
PRIOR FILING DATE: 2002-01-15	Qy	1202	TCCTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTGTGAAATG	1261
PRIOR APPLICATION NUMBER: 60/059263	Db	841	TCCTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTGTGAAATG	900
PRIOR FILING DATE: 1997-09-18	Qy	1262	GTGACACAAATCTCGCCATGATCTCAGTACCTTTATCAAGAGGTTGTGGGAAGAAATGAT	1321
PRIOR APPLICATION NUMBER: 60/062250	Db	901	GTGACACAAATCTCGCCATGATCTCAGTACCTTTATCAAGAGGTTGTGGGAAGAAATGAT	960
PRIOR FILING DATE: 1997-10-17	Qy	1322	AGAAGGGAGCCGGGACACACAAATGATGTCCTTTGAAGAAATGAACAACCTCTCAGCACCTG	1381
PRIOR APPLICATION NUMBER: 60/063120	Db	961	AGAAGGGAGCCGGGACACACAAATGATGTCCTTTGAAGAAATGAACAACCTCTCAGCACCTG	1020
PRIOR FILING DATE: 1997-10-24	Qy	1382	TCATGTCCTCAGTAGAAGTTGTGAAACCAAGCTGTCAAGAAATCTTTGAAACACATCC	1441
PRIOR APPLICATION NUMBER: 60/063541	Db	1021	TCATGTCCTCAGTAGAAGTTGTGAAACCAAGCTGTCAAGAAATCTTTGAAACACATCC	1080
PRIOR FILING DATE: 1997-10-28	Qy	1442	ATGGCAAAACAGCTTTTAATACACACTTTGAGATGGAGGAGTTATAAAGAAATGTCACAG	1501
PRIOR APPLICATION NUMBER: 60/063544	Db	1081	ATGGCAAAACAGCTTTTAATACACACTTTGAGATGGAGGAGTTATAAAGAAATGTCACAG	1140
PRIOR FILING DATE: 1997-10-28	Qy	1502	AAGAAAACACAAACCTTTGTTTACTGGAATTTTGTGAAATTTTGTAGTACATATGTTT	1561
PRIOR APPLICATION NUMBER: 60/063544	Db	1141	AAGAAAACACAAACCTTTGTTTACTGGAATTTTGTGAAATTTTGTAGTACATATGTTT	1200
PRIOR FILING DATE: 1997-10-28	Qy	1562	CAGAAATATGTAGAAATAAAATGTTGCCATATAAATAACACCTTACATATATCTA	1621
PRIOR APPLICATION NUMBER: 60/063544	Db	1201	CAGAAATATGTAGAAATAAAATGTTGCCATATAAATAACACCTTACATATATCTA	1260
PRIOR FILING DATE: 1997-10-28	Qy	1622	TGCTTTTAAATGAGGATGGAAGATTTTCAATGTCATAAGTCAACCTCGGACAAATTTGA	1681
PRIOR APPLICATION NUMBER: 60/063544	Db	1261	TGCTTTTAAATGAGGATGGAAGATTTTCAATGTCATAAGTCAACCTCGGACAAATTTGA	1320
PRIOR FILING DATE: 1997-10-28	Qy	1682	TGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCTGTGTATGACTTTTA	1741
PRIOR APPLICATION NUMBER: 60/063544	Db	1321	TGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCTGTGTATGACTTTTA	1380
PRIOR FILING DATE: 1997-10-28	Qy	1742	CTGAACACAGTATGTTTGGAGCAGCATGTTTGTAGTATGATTTCCGATCCATCCAAA	1801
PRIOR APPLICATION NUMBER: 60/063544	Db	1381	CTGAACACAGTATGTTTGGAGCAGCATGTTTGTAGTATGATTTCCGATCCATCCAAA	1440
PRIOR FILING DATE: 1997-10-28	Qy	1802	CGAGTACATATGCTGGGACTGGAGCATAAGTAAAGTTGATTTACTTTTACCAACTAGT	1861
PRIOR APPLICATION NUMBER: 60/063544	Db	1441	CGAGTACATATGCTGGGACTGGAGCATAAGTAAAGTTGATTTACTTTTACCAACTAGT	1500
PRIOR FILING DATE: 1997-10-28	Qy	1862	ATATAAGTACTAATTAATGCTAATAGGAGTTAGAAATACATACTAATTTTATTA	1921

APPLICANT: Goddard, Audrey	Qy	362	AGAGAAAGAGCGTCTCCAGTGAAGCAATGCGAGCCCTCGGCTCTCCGCGAAGAGTT	421
APPLICANT: Godowski, Paul J.	Db	1	AGAGAAAGAGCGTCTCCAGTGAAGCAATGCGAGCCCTCGGCTCTCCGCGAAGAGTT	60
APPLICANT: Gurney, Austin L.	Qy	422	CCCTGCCCGATGAGCCCGCGCTGCTCCCGACTATCCCGAGGCGGCGTGGCGAC	481
APPLICANT: Pan, James	Db	61	CCCTGCCCGATGAGCCCGCGCTGCTCCCGACTATCCCGAGGCGGCGTGGCGAC	120
APPLICANT: Smith, Victoria	Qy	482	CGGGCCCGAGCGCGACGATCGCTGCGGTTTTCCTTGGAGTAGGATGTTGGTGAAGGA	541
APPLICANT: Watanabe, Colin K.	Db	121	CGGGCCCGAGCGCGACGATCGCTGCGGTTTTCCTTGGAGTAGGATGTTGGTGAAGGA	180
APPLICANT: Wood, William I.	Qy	542	TGGGCTTCTCCCTTACCGGCTCACAATGCGCAGAGAGATTCGTTGAAGTGTGCGC	601
APPLICANT: Zhang, Zemin	Db	181	TGGGCTTCTCCCTTACCGGCTCACAATGCGCAGAGAGATTCGTTGAAGTGTGCGC	240
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	Qy	602	TGCTGTCTACGCGCTCAATCTGCTCTTTTGGTTTAAATGTCATCCAGTGTGCGAGTT	661
TITLE OF INVENTION: ACIDS ENCODING THE SAME	Db	241	TGCTGTCTACGCGCTCAATCTGCTCTTTTGGTTTAAATGTCATCCAGTGTGCGAGTT	300
FILE REFERENCE: P3430R1C465	Qy	662	TCTGTTGGATGAGGAGTACTAAATATGTTCTCACTTTAACTGCGAAGAGGGA	721
CURRENT APPLICATION NUMBER: US/10/201.853	Db	301	TCTGTTGGATGAGGAGTACTAAATATGTTCTCACTTTAACTGCGAAGAGGGA	360
PRIOR FILING DATE: 2002-07-23	Qy	722	GAGGAAGCAGTCATTTTCACTTCTCTGCTGCTTCAATCGGTCATCGATGCTGTTTC	781
PRIOR APPLICATION NUMBER: 10/052586	Db	361	GAGGAAGCAGTCATTTTCACTTCTCTGCTGCTTCAATCGGTCATCGATGCTGTTTC	420

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-10-201-853-323

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US-10-201-853-323

US-10-201-853-323

US-10-201-853-323

US-10-201-853-323

US-10-201-853-323

Db 1501 ATATAAGTCTAATTAATGCTAATAGTAACTAGAGTGTAGAAATACATACTAATCTTTATTA 1560
Qy 1922 CTGAGCGATCTATCTCTGATGCTAAATAATATATATATACAGAAATCTTTCAATATGG 1981
Db 1561 CTGAGCGATCTATCTCTGATGCTAAATAATATATATATACAGAAATCTTTCAATATGG 1620
Qy 1982 TGACTACCTAAATGATGATTTTGTGCTGCTAATAATATCTTACCACTTTAAAGACAA 2041
Db 1621 TGACTACCTAAATGATGATTTTGTGCTGCTAATAATATCTTACCACTTTAAAGACAA 1680
Qy 2042 GCTAACACATGCTTTAAGCTGATCAGGATTTTTCGTATATAGTCTGTGTTAAATCTG 2101
Db 1681 GCTAACACATGCTTTAAGCTGATCAGGATTTTTCGTATATAGTCTGTGTTAAATCTG 1740
Qy 2102 TATAATTCAGTCGATTTTCACTGCTAATAATGTTAAGATTAACCATTAAGAAAGGAAT 2161
Db 1741 TATAATTCAGTCGATTTTCACTGCTAATAATGTTAAGATTAACCATTAAGAAAGGAAT 1800
Qy 2162 TTGCTCTGTATAGCATCATTTATTTTACGCTTTTCTGTTAATAAGCTTTTACTATTTCTGT 2221
Db 1801 TTGCTCTGTATAGCATCATTTATTTTACGCTTTTCTGTTAATAAGCTTTTACTATTTCTGT 1860
Qy 2222 CCTGGCTTATATACACATATACCTGTTTATTAATATCTTACCCTAATTTTGAAT 2281
Db 1861 CCTGGCTTATATACACATATACCTGTTTATTAATATCTTACCCTAATTTTGAAT 1920
Qy 2282 TACCAGTGTGATACATAGGAATCATTTATCAGATGATGCTGCTTTTAAAGGATTA 2341
Db 1921 TACCAGTGTGATACATAGGAATCATTTATCAGATGATGCTGCTTTTAAAGGATTA 1980
Qy 2342 ATAGAATAATTTGACATACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTCTCC 2401
Db 1981 ATAGAATAATTTGACATACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTCTCC 2040
Qy 2402 CAATGAAGACTCTTTTGTACATTAACACTTTTAAAGGCTTATCTTTCCTCTCCA 2461
Db 2041 CAATGAAGACTCTTTTGTACATTAACACTTTTAAAGGCTTATCTTTCCTCTCCA 2100
Qy 2462 AACAGAAGCAATAGTCTCCAAGTCAATATAAATCTTACAGAAATAGTGTCTTTTCT 2521
Db 2101 AACAGAAGCAATAGTCTCCAAGTCAATATAAATCTTACAGAAATAGTGTCTTTTCT 2160
Qy 2522 CCAGAAATGCTTGTGAGATCAATTAACATGTCACATTTAGAGATCTTTGTTT 2581
Db 2161 CCAGAAATGCTTGTGAGATCAATTAACATGTCACATTTAGAGATCTTTGTTT 2220
Qy 2582 TTTCACCTGATTAATATATCTGTCGCAATTAACAGATTAATAATTTTACAGAGTA 2641
Db 2221 TTTCACCTGATTAATATATCTGTCGCAATTAACAGATTAATAATTTTACAGAGTA 2280
Qy 2642 TAGTATATTTATTTGAATGGAAAGTGCATTTTACTGATTTTGTGATTTTGTAT 2701
Db 2281 TAGTATATTTATTTGAATGGAAAGTGCATTTTACTGATTTTGTGATTTTGTAT 2340
Qy 2702 TTCTCAGAAATGGAAGAAATTAATAATGTCGCAATATAATTTTCTAGAGAGTA 2758
Db 2341 TTCTCAGAAATGGAAGAAATTAATAATGTCGCAATATAATTTTCTAGAGAGTA 2397

RESULT 9

US-10-063-745-107

; Sequence 107, Application US/10063745

; Publication No. US20040058411A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,745
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 107
LENGTH: 2397
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-745-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	362	AGAGAAAGACGCTCCAGCTGAAGCCAAATGCAACCTCCGCTCTCCGCAAGAAATGTT	421
Db	1	AGAGAAAGACGCTCCAGCTGAAGCCAAATGCAACCTCCGCTCTCCGCAAGAAATGTT	60
Qy	422	CCCTGCCCGGATGAGCCCGCGCTGCGTCCCGACTATCCCAAGCGGCGTGGGCAC	481
Db	61	CCCTGCCCGGATGAGCCCGCGCTGCGTCCCGACTATCCCAAGCGGCGTGGGCAC	120
Qy	482	CGGCGCCAGCCGCGACGATCGCTGCCGTTTTCGCTTTGGGAGTAGGATGTGTTGAAAGGA	541
Db	121	CGGCGCCAGCCGCGACGATCGCTGCCGTTTTCGCTTTGGGAGTAGGATGTGTTGAAAGGA	180
Qy	542	TGGGCTTCTCCCTTACCGGCTCACAATGCGGCGAGAGAGATTCGTTGAAGTGTCTGGC	601
Db	181	TGGGCTTCTCCCTTACCGGCTCACAATGCGGCGAGAGATTCGTTGAAGTGTCTGGC	240
Qy	602	TGCTGTCTACGCGCTCAATCTGCTCTTTTGTGTAAATGTCCATCAGTGTGTTGGCAGTT	661
Db	241	TGCTGTCTACGCGCTCAATCTGCTCTTTTGTGTAAATGTCCATCAGTGTGTTGGCAGTT	300
Qy	662	TCTGCTTGGATGAGGAGCTACTAAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	721
Db	301	TCTGCTTGGATGAGGAGCTACTAAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	360
Qy	722	GAGGAGCAGTCATTTGACCTTACTTCTCTGCTGTTTCAATCGGTCATGATTTGCTGTTTC	781
Db	361	GAGGAGCAGTCATTTGACCTTACTTCTCTGCTGTTTCAATCGGTCATGATTTGCTGTTTC	420
Qy	782	TGTTTCTTATCATTTGGGATGTTAGGATATTGTGAAACGTTGAAAGAAATCTGTTG	841
Db	421	TGTTTCTTATCATTTGGGATGTTAGGATATTGTGAAACGTTGAAAGAAATCTGTTG	480
Qy	842	CTTCTTGATGCTACTTTGGAAGTTTCTGTCATTTTCTGTTAGAACTGCTGTTGGC	901
Db	481	CTTCTTGATGCTACTTTGGAAGTTTCTGTCATTTTCTGTTAGAACTGCTGTTGGC	540
Qy	902	GTTTGGACATATGAACGAACTTATGTTCCAGTACAATGCTCAGATATGTTGTCATTTG	961
Db	541	GTTTGGACATATGAACGAACTTATGTTCCAGTACAATGCTCAGATATGTTGTCATTTG	600
Qy	962	AAAGCAGGATGACAAATATGATGATATGATATCGTGGCTTACTCATGCTTGGAAAT	1021
Db	601	AAAGCAGGATGACAAATATGATGATATGATATCGTGGCTTACTCATGCTTGGAAAT	660
Qy	1022	TTTTTTCAGAGAGAGTTTAAAGTGTGTTGAGTATATTTTCACTGCTGTTGGAATG	1081
Db	661	TTTTTTCAGAGAGAGTTTAAAGTGTGTTGAGTATATTTTCACTGCTGTTGGAATG	720
Qy	1082	ACAGAGATGAGCTGGCCCCAGATTTCTGCTGTTGTTAGAAATTTCCAGAGATGTTTCAA	1141
Db	721	ACAGAGATGAGCTGGCCCCAGATTTCTGCTGTTGTTAGAAATTTCCAGAGATGTTTCAA	780
Qy	1142	CAGGCCACACAGGAGATCTCAGTGACCTTTTATCAAGAGGTTTGTGGGAGAAATGAT	1201
Db	781	CAGGCCACACAGGAGATCTCAGTGACCTTTTATCAAGAGGTTTGTGGGAGAAATGAT	840

QY 1202 TCCTTTTGGAGGAAACCAAACTGCGGTGCTGAGGTGTTCTGGGAATCTCCATTGGG 1261
Db 841 TCCTTTTGGAGGAAACCAAACTGCGGTGCTGAGGTGTTCTGGGAATCTCCATTGGG 900
QY 1262 GTGACAAATCTGGCCATGATTCCTCAACATCTGCTGCGGCTCTGTATATGAT 1321
Db 901 GTGACAAATCTGGCCATGATTCCTCAACATCTGCTGCGGCTCTGTATATGAT 960
QY 1322 AGAAGGAGCGGGGAGAGCAAACTGCTGAGGATGAGGATGAGGATGAGGATGAGGAT 1381
Db 961 AGAAGGAGCGGGGAGAGCAAACTGCTGAGGATGAGGATGAGGATGAGGATGAGGAT 1020
QY 1382 TCATGTCCTCTGAGTAACTGTTGAAACCAAGCTGTCAAGAACTCTTGAACACATCC 1441
Db 1021 TCATGTCCTCTGAGTAACTGTTGAAACCAAGCTGTCAAGAACTCTTGAACACATCC 1080
QY 1442 ATGCAAAACAGCTTAAATACACACTTTGAGTGGAGGATTAATAAGAAAGTGTACAG 1501
Db 1081 ATGCAAAACAGCTTAAATACACACTTTGAGTGGAGGATTAATAAGAAAGTGTACAG 1140
QY 1502 AAGAAACCAAACTGTTTAACTGAGCTGTGAAATTTTGGATGATCACTATGTTT 1561
Db 1141 AAGAAACCAAACTGTTTAACTGAGCTGTGAAATTTTGGATGATCACTATGTTT 1200
QY 1562 CAGAAATATGTAGAAATATAAAATGTTGCCATAAAATACCACTTAAGCATATCTATCTA 1621
Db 1201 CAGAAATATGTAGAAATATAAAATGTTGCCATAAAATACCACTTAAGCATATCTATCTA 1260
QY 1622 TGCTTTAAATGAGGATGAAAGTTCATGTCATAGTCACCACTGGACCAATAATGTA 1681
Db 1261 TGCTTTAAATGAGGATGAAAGTTCATGTCATAGTCACCACTGGACCAATAATGTA 1320
QY 1682 TGCCCTTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTATGACTTTA 1741
Db 1321 TGCCCTTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTATGACTTTA 1380
QY 1742 CTGAACACAGTATGTTTGGAGGAGCATGTTGATTTAGCATTTCCGCACTCCAGAA 1801
Db 1381 CTGAACACAGTATGTTTGGAGGAGCATGTTGATTTAGCATTTCCGCACTCCAGAA 1440
QY 1802 CGAGTCATATGTTGGGAGCTGGAGCCATAGTAAAGGTTCATTTTCTTACCAACTAGT 1861
Db 1441 CGAGTCATATGTTGGGAGCTGGAGCCATAGTAAAGGTTCATTTTCTTACCAACTAGT 1500
QY 1862 ATATAAGTACTAAATTAAGTCTAACATAGGAAGTTAGAAATTAATTAATTAATTA 1921
Db 1501 ATATAAGTACTAAATTAAGTCTAACATAGGAAGTTAGAAATTAATTAATTAATTA 1560
QY 1922 CTCAGCGATCTATCTCTGATGCTAAATTAATTAATTAATTAATTAATTAATTAAT 1981
Db 1561 CTCAGCGATCTATCTCTGATGCTAAATTAATTAATTAATTAATTAATTAATTAAT 1620
QY 1982 TGACTACCTAAATGTGATTTTGTGCTGTTACTAAATTAATTTCTTACCCTTAAAGAGCAA 2041
Db 1621 TGACTACCTAAATGTGATTTTGTGCTGTTACTAAATTAATTTCTTACCCTTAAAGAGCAA 1680
QY 2042 GCTAACACATGCTTAAAGTCTAGCAGGATTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db 1681 GCTAACACATGCTTAAAGTCTAGCAGGATTTTGTATATAAGTCTGTGTTAAATCTG 1740
QY 2102 TATAATTCAGTCGATTTTCAGTTCCTGATAATGTTAAGAAATACCACTTATGAAAGGAAAT 2161
Db 1741 TATAATTCAGTCGATTTTCAGTTCCTGATAATGTTAAGAAATACCACTTATGAAAGGAAAT 1800
QY 2162 TTGTCCTGTAAGATCAATTAATTTTACCTTTTCTGTTTAAATGCTTTTACTTTCTGT 2221
Db 1801 TTGTCCTGTAAGATCAATTAATTTTACCTTTTCTGTTTAAATGCTTTTACTTTCTGT 1860
QY 2222 CCTGGGCTTATATACATATACTGTTATTTAAATTAATTTAAACCTAATTTTGAAT 2281
Db 1861 CCTGGGCTTATATACATATACTGTTATTTAAATTAATTTAAACCTAATTTTGAAT 1920

QY 2282 TACCAGTGTGATACATAGGAATCATATTATCAGATGTAGTCTGTTTACGAAGTATTA 2341
Db 1921 TACCAGTGTGATACATAGGAATCATATTATCAGATGTAGTCTGTTTACGAAGTATTA 1980
QY 2342 ATAGAAATTTGACATAACTTATGATTCAGAAAGGACTGTATCTGTTTCTCC 2401
Db 1981 ATAGAAATTTGACATAACTTATGATTCAGAAAGGACTGTATCTGTTTCTCC 2040
QY 2402 CAAATGAAGACTCTTTTGGACACTAAACACTTTTAAAGCTTATCTTGCCTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTGGACACTAAACACTTTTAAAGCTTATCTTGCCTCTCCA 2100
QY 2462 AACAGAGCAATAGTCTCCAGTCATATTAATTTCTACAGAAATAGTCTTCTTTCT 2521
Db 2101 AACAGAGCAATAGTCTCCAGTCATATTAATTTCTACAGAAATAGTCTTCTTTCT 2160
QY 2522 CCAGAAATGCTTCTGAGAACTCAATTAATTAATTTAGAGATTTCTTCTTTT 2581
Db 2161 CCAGAAATGCTTCTGAGAACTCAATTAATTAATTTAGAGATTTCTTCTTTT 2220
QY 2582 TTCTACTGATTAATATCTGTGGCAAAATACAGATTAATTAATTTTACAGAGTA 2641
Db 2221 TTCTACTGATTAATATCTGTGGCAAAATACAGATTAATTAATTTTACAGAGTA 2280
QY 2642 TAGTATATTTTGAATGGAAGTGCATTTTCTGTTTCTGTTTCTTTT 2701
Db 2281 TAGTATATTTTGAATGGAAGTGCATTTTCTGTTTCTGTTTCTTTT 2340
QY 2702 TTCTCAGAAATGGAAGAAATTAATTAATTTCTCAATTAATTTTCTAGAGTAA 2758
Db 2341 TTCTCAGAAATGGAAGAAATTAATTAATTTCTCAATTAATTTTCTAGAGTAA 2397

RESULT 10
US-10-063-512-107
; Sequence 107, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Estor, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 362 AGAAGAAAGAGCGTCTCCAGCTGAAAGCCCAATCAGCCCTCCGGCTCTCCGCGAAGAGTT 421
Db 1 AGAAGAAAGAGCGTCTCCAGCTGAAAGCCCAATCAGCCCTCCGGCTCTCCGCGAAGAGTT 60
QY 422 CCTGCCCCGATAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGGCGTGGGCGAC 481
Db 61 CCTGCCCCGATAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGGCGTGGGCGAC 120
QY 482 CGGCCCCGAGCGCGAGCATCGTGGCTTTTGGCTTGGAGTAGGATGTGTGAGAGGA 541

2702	TCTCAGAAATATGAAAAGAAATTTAAATGTGTCAATAAATATTTTCTAGAGAGTAA	2758
2341	TCTCAGAAATATGAAAAGAAATTTAAATGTGTCAATAAATATTTTCTAGAGAGTAA	2397

RESULT 11					
US-10-063-513-107					
; Sequence 107, Application US/10063513					
; Publication No. US20030018172A1					
; GENERAL INFORMATION:					
; APPLICANT: Eaton, Dan L.					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Geritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Grimaldi, Christopher J.					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Watanabe, Colin K.					
; APPLICANT: Wood, William I.					
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC					
; FILE REFERENCE: P3230R1C1					
; CURRENT APPLICATION NUMBER: US/10/063.513					
; CURRENT FILING DATE: 2002-05-01					
; Prior Application removed - See File Wrapper or Palm					
; NUMBER OF SEQ ID NOS: 170					
; SEQ ID NO 107					
; LENGTH: 2397					
; TYPE: DNA					
; ORGANISM: Homo Sapien					
US-10-063-513-107					
Query Match 86.5%; Score 2393.8; DB 13; Length 2397;					
Best Local Similarity 99.9%; Pred No. 0;					
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	362	AGAGAAAGAAGCGTCTCCAGCTGGAAGCAATGCAGCCCTCCGGCTCTCCGGCGAAGAAGTT	421		
DB	1	AGAGAAAGAAGCGTCTCCAGCTGGAAGCAATGCAGCCCTCCGGCTCTCCGGCGAAGAAGTT	60		
QY	422	CCCTGCCCGTAGAGCCCCCGCGTGCGTCCCAGACTATCCCAGCGGGCGGTGGGGCAC	481		
DB	61	CCCTGCCCGTAGAGCCCCCGCGTGCGTCCCAGACTATCCCAGCGGGCGGTGGGGCAC	120		
QY	482	CGGGCCACGCGCCGACATCGCTGCCGTTTTGCCCTTGGAGTAGAGTGTGGTGAAGAAG	541		
DB	121	CGGGCCACGCGCCGACATCGCTGCCGTTTTGCCCTTGGAGTAGAGTGTGGTGAAGAAG	180		
QY	542	TGGGGCTTCCTCTTACGGGGCTACAATGGCCAGAGAGATCCGTCGAAGTGTCTGGC	601		
DB	181	TGGGGCTTCCTCTTACGGGGCTACAATGGCCAGAGAGATCCGTCGAAGTGTCTGGC	240		
QY	602	TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTTAATCTCCATCAGTGTGTGGCAGTT	661		
DB	241	TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTTAATCTCCATCAGTGTGTGGCAGTT	300		
QY	662	TCGTGTGATGAGGAGCTACCTAAATATGTTCTCACTTTAACTGCAGAACCGAGGTA	721		
DB	301	TCGTGTGATGAGGAGCTACCTAAATATGTTCTCACTTTAACTGCAGAACCGAGGTA	360		
QY	722	GAGGAAGCAGTCATTITGACTTACTTTCTCTGGTTTCATCCGGTTCATGTTGCTTTTGC	781		
DB	361	GAGGAAGCAGTCATTITGACTTACTTTCTCTGGTTTCATCCGGTTCATGTTGCTTTTGC	420		
QY	782	TGTTTCTTATCATCTGGGGAGTTAGGATATTTGGGAACCGTGAAAAGAAATCTGTTG	841		
DB	421	TGTTTCTTATCATCTGGGGAGTTAGGATATTTGGGAACCGTGAAAAGAAATCTGTTG	480		
QY	842	CTTCTTGATGTPACTTTTGAAGTTTGGTTTGCATTCTTCTGTGTAGAACTGGCTTTGGC	901		
DB	481	CTTCTTGATGTPACTTTTGAAGTTTGGTTTGCATTCTTCTGTGTAGAACTGGCTTTGGC	540		

Db 1621 TGACTACCAATGTAATTTTGTGGTACTAAATATATCTTACCACCTTAAAGAGCAA 1680
Qy 2042 GCTAACACATTTGCTTAAGCTGATCAGGATTTTGTATATAGTCTGTGTTAAATCTG 2101
Db 1681 GCTAACACATTTGCTTAAGCTGATCAGGATTTTGTATATAGTCTGTGTTAAATCTG 1740
Qy 2102 TATATTCAGTCGATTTTCAAGTCTGATAATGTTAAGAAATAACCATTTATGAAGAGAAAT 2161
Db 1741 TATATTCAGTCGATTTTCAAGTCTGATAATGTTAAGAAATAACCATTTATGAAGAGAAAT 1800
Qy 2162 TTGTCCTGTATAGCATCATTTATTTTGTAGCTTTTCCCTGTTTAAAGCTTTTACTATCTGT 2221
Db 1801 TTGTCCTGTATAGCATCATTTATTTTGTAGCTTTTCCCTGTTTAAAGCTTTTACTATCTGT 1860
Qy 2222 CCTGGCTTATATTAACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2281
Db 1861 CCTGGCTTATATTAACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 1920
Qy 2282 TACCAGTGTATATTAACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2341
Db 1921 TACCAGTGTATATTAACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 1980
Qy 2342 ATAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2401
Db 1981 ATAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2040
Qy 2402 CAATGAAGACTCTTTTGTAGCATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2461
Db 2041 CAATGAAGACTCTTTTGTAGCATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2100
Qy 2462 AACAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2521
Db 2101 AACAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2160
Qy 2522 CCAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2581
Db 2161 CCAGAAATTTTGCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2220
Qy 2582 TTTCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2641
Db 2221 TTTCACATATTAATCTGTTATTTTAAATTAACCACTAAATTTTGAAT 2280
Qy 2642 TAGTATATTTTATTTGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2701
Db 2281 TAGTATATTTTATTTGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2340
Qy 2702 TTCTCAGATATGGAAGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2758
Db 2341 TTCTCAGATATGGAAGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2397

RESULT 12

US-10-063-549-107
; Sequence 107, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: E230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 107.
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-549-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 AGAGAAAGAGGCTCTCAGCTGAAGCAATGCGCCCTCGGCTCTCCGCGAAGATT 421
Db 1 AGAGAAAGAGGCTCTCAGCTGAAGCAATGCGCCCTCGGCTCTCCGCGAAGATT 60
Qy 422 CCTGCCCCGATGAGCCCCCGGCTGCTCCCGACTATCCCCAGGCGGCGTGGGCGAC 481
Db 61 CCTGCCCCGATGAGCCCCCGGCTGCTCCCGACTATCCCCAGGCGGCGTGGGCGAC 120
Qy 482 CGGCGCCAGCGCCGACGATCGCTGCTTTTCCCTTTGGGAGTAGGATGTTGTAAGGA 541
Db 121 CGGCGCCAGCGCCGACGATCGCTGCTTTTCCCTTTGGGAGTAGGATGTTGTAAGGA 180
Qy 542 TGGGCTTCTCCCTTACCGGGCTCACAATGCGCCAGAGAGATTCCGTGAAGTGTCTGGC 601
Db 181 TGGGCTTCTCCCTTACCGGGCTCACAATGCGCCAGAGAGATTCCGTGAAGTGTCTGGC 240
Qy 602 TGCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCATCATGTTGGCAGTT 661
Db 241 TGCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCATCATGTTGGCAGTT 300
Qy 662 TCTGCTTGGTAGGAGCTACTTAATAATGTTCTCTCACTTTTCTGAGAGAAACGAGGTA 721
Db 301 TCTGCTTGGTAGGAGCTACTTAATAATGTTCTCTCACTTTTCTGAGAGAAACGAGGTA 360
Qy 722 GAGGAGCAGTCATTTTGTACTTCTCTGTTGTTTCTCCGCTCATGTTGTTGTTG 781
Db 361 GAGGAGCAGTCATTTTGTACTTCTCTGTTGTTTCTCCGCTCATGTTGTTGTTG 420
Qy 782 TGTTCCTTATCATTTGTTGGGAGTTAGGATTTTGTGAGAACTGTTGTTGTTG 841
Db 421 TGTTCCTTATCATTTGTTGGGAGTTAGGATTTTGTGAGAACTGTTGTTGTTG 480
Qy 842 CTTCCTGATGCTATTTTGAAGTTTCTGCTCATTTTCTGTTGAGAACTGTTGTTG 901
Db 481 CTTCCTGATGCTATTTTGAAGTTTCTGCTCATTTTCTGTTGAGAACTGTTGTTG 540
Qy 902 GTTTGGACATATGAACAGGAACTTATGTTCCAGTACAAATGTTGTTGTTGTTG 961
Db 541 GTTTGGACATATGAACAGGAACTTATGTTCCAGTACAAATGTTGTTGTTGTTG 600
Qy 962 AAAGCCAGGATGACAAATTTTGAATTTTCTGTTGTTGTTGTTGTTGTTGTTG 1021
Db 601 AAAGCCAGGATGACAAATTTTGAATTTTCTGTTGTTGTTGTTGTTGTTGTTG 660
Qy 1022 TTTTTCAGAGAGATTTTAAAGTCTGTTGAGTAGTATATTTTCTGCTGTTGTTGTTG 1081
Db 661 TTTTTCAGAGAGATTTTAAAGTCTGTTGAGTAGTATATTTTCTGCTGTTGTTGTTG 720
Qy 1082 ACAGAGATGAGTGGCCCCCAGATTTCTGCTGTTGTTGAGAAATTTCCAGATGTTCCAA 1141
Db 721 ACAGAGATGAGTGGCCCCCAGATTTCTGCTGTTGTTGAGAAATTTCCAGATGTTCCAA 780
Qy 1142 CAGGCCACCCAGGAAAGTCTCAGTGAACCTTTATCAAGAGGTTTGTGGGAGAAATTTAT 1201
Db 781 CAGGCCACCCAGGAAAGTCTCAGTGAACCTTTATCAAGAGGTTTGTGGGAGAAATTTAT 840
Qy 1202 TCCTTTTGTAGAGAGAAACCAACTGCTGAGGTTTCTGAGGTTTCTGGGATTTCTCATTTGG 1261
Db 841 TCCTTTTGTAGAGAGAAACCAACTGCTGAGGTTTCTGAGGTTTCTGGGATTTCTCATTTGG 900
Qy 1262 GTGACACAAATCTGCGCATGTTTCTCAGCATTTCTGCTCTGGGCTCTGTATTATGAT 1321
Db 901 GTGACACAAATCTGCGCATGTTTCTCAGCATTTCTGCTCTGGGCTCTGTATTATGAT 960

QY 1322 AGAAGGAGCGGGGACAGACCAAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
DB 961 AGAAGGAGCGCTGGGACAGACCAAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020
QY 1382 TCATGTCCTCAGTAGAAGCTGTTGAACCAAGGCTGTCAAGAACTCTTGAACACACATCC 1441
DB 1021 TCATGTCCTCAGTAGAAGCTGTTGAACCAAGGCTGTCAAGAACTCTTGAACACACATCC 1080
QY 1442 ATGGCAAAACAGCTTTAATACACACTTTGAGATGGAGAGTTATAAAAGAAATGTCCACAG 1501
DB 1081 ATGGCAAAACAGCTTTAATACACACTTTGAGATGGAGAGTTATAAAAGAAATGTCCACAG 1140
QY 1502 AAGAAAACCAAACTGTTTACTGCACTGTGTAATTTTGTAGTACATCTATGTTT 1561
DB 1141 AAGAAAACCAAACTGTTTACTGCACTGTGTAATTTTGTAGTACATCTATGTTT 1200
QY 1562 CAGAAATATGTAAGAAATTAAGAAATGTCCTAATAAATACCACTTAAAGCAATATCTTCTA 1621
DB 1201 CAGAAATATGTAAGAAATTAAGAAATGTCCTAATAAATACCACTTAAAGCAATATCTTCTA 1260
QY 1622 TGCTTTAAATGAGGATGGAAGAGTTTCATGTCATAGTCACCACTGGCAATATGTA 1681
DB 1261 TGCTTTAAATGAGGATGGAAGAGTTTCATGTCATAGTCACCACTGGCAATATGTA 1320
QY 1682 TGCCCTTAAATGCTGAAGACAGATGTCATACCACCTGTAGCTGTGATGACTTTTA 1741
DB 1321 TGCCCTTAAATGCTGAAGACAGATGTCATACCACCTGTAGCTGTGATGACTTTTA 1380
QY 1742 CTGAACACAGTATGTTTGGAGGAGCATGTTTGAATAGCAATTCGGCATCCATGCAAA 1801
DB 1381 CTGAACACAGTATGTTTGGAGGAGCATGTTTGAATAGCAATTCGGCATCCATGCAAA 1440
QY 1802 CGAGTCATATGTTGGAGCTGGAGCCATAGTAAAGTTGATTTACTTTTACCAACTAGT 1861
DB 1441 CGAGTCATATGTTGGAGCTGGAGCCATAGTAAAGTTGATTTACTTTTACCAACTAGT 1500
QY 1862 ATATAAGTACTAATTAAGTCTAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 1921
DB 1501 ATATAAGTACTAATTAAGTCTAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 1560
QY 1922 CTCAGCGATCTATCTCTGATGCTAAATATAATATATATATATATATATATATATATATAT 1981
DB 1561 CTCAGCGATCTATCTCTGATGCTAAATATAATATATATATATATATATATATATATATAT 1620
QY 1982 TGACTACCTAAATGATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2041
DB 1621 TGACTACCTAAATGATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1680
QY 2042 GCTAACACATGCTTAAAGCTGATCAGGAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2101
DB 1681 GCTAACACATGCTTAAAGCTGATCAGGAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1740
QY 2102 TATAATTCAGTCGATTCAGTCTGATAATGTTAAGAAATACCAATATGAAAGGAAAT 2161
DB 1741 TATAATTCAGTCGATTCAGTCTGATAATGTTAAGAAATACCAATATGAAAGGAAAT 1800
QY 2162 TTGTCTCTGATAGCATATATTTTACGCTTCTCTGTTAATTAAGCTTTTACTATTCCTGT 2221
DB 1801 TTGTCTCTGATAGCATATATTTTACGCTTCTCTGTTAATTAAGCTTTTACTATTCCTGT 1860
QY 2222 CCTGGGCTTATATACACATATACTGTTATTTAAATACCTTAAACCACTAATTTTGAAGAT 2281
DB 1861 CCTGGGCTTATATACACATATACTGTTATTTAAATACCTTAAACCACTAATTTTGAAGAT 1920
QY 2282 TACAGTGTGATACATAGGAATCATTTTACAGATGATGCTGCTTTTACTAGGATTTA 2341
DB 1921 TACAGTGTGATACATAGGAATCATTTTACAGATGATGCTGCTTTTACTAGGATTTA 1980
QY 2342 ATAGAAAATTTGACATAAATAGTTGATTCAGAAAAGCACTTGTATGCTGTTTTTCTCC 2401
DB 1981 ATAGAAAATTTGACATAAATAGTTGATTCAGAAAAGCACTTGTATGCTGTTTTTCTCC 2040

QY 2402 CAAATGAAGACTCTTTTGGACACTAAACACTTTTAAAGAGCTTATCTTGCCTTCTCCA 2461
DB 2041 CAAATGAAGACTCTTTTGGACACTAAACACTTTTAAAGAGCTTATCTTGCCTTCTCCA 2100
QY 2462 AACAAAGAGCAATAGTCTCCAAAGTCAATATAAAATCTACAGAAAATAGTGTCTTTTCT 2521
DB 2101 AACAAAGAGCAATAGTCTCCAAAGTCAATATAAAATCTACAGAAAATAGTGTCTTTTCT 2160
QY 2522 CCAGAAAATGCTTGTGAGAATCATTTAAACATGTGACAAATTTAGAGATCTTTGTTTTA 2581
DB 2161 CCAGAAAATGCTTGTGAGAATCATTTAAACATGTGACAAATTTAGAGATCTTTGTTTTA 2220
QY 2582 TTTCTACTGATTAATATCTGTGGCAAAATTTACACAGATTTAAATTTTTCACAGAGTA 2641
DB 2221 TTTCTACTGATTAATATCTGTGGCAAAATTTACACAGATTTAAATTTTTCACAGAGTA 2280
QY 2642 TAGTATATTTTTCAGAAATGGGAAAGTGCATTTTACTGTATTTTGTGTATTTTGTAT 2701
DB 2281 TAGTATATTTTTCAGAAATGGGAAAGTGCATTTTACTGTATTTTGTGTATTTTGTAT 2340
QY 2702 TTTCTCAGAAATATGGAAGAAATTTAAATGTGTCAATAAATTTTTCAGAGAGTAA 2758
DB 2341 TTTCTCAGAAATATGGAAGAAATTTAAATGTGTCAATAAATTTTTCAGAGAGTAA 2397

RESULT 13

US-10-063-569-107
; Sequence 107, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 362 AGAGAAAGAGGCTCTCCAGCTGAAGCCCAATCAGCCCTCCGCTCTCCGCGAAGATT 421
DB 1 AGAGAAAGAGGCTCTCCAGCTGAAGCCCAATCAGCCCTCCGCTCTCCGCGAAGATT 60
QY 422 CCTGCCCCGATGAGCCCCCGGCTGCCGCTCCGCTATCCCGAGCGGCGTGGGCGAC 481
DB 61 CCTGCCCCGATGAGCCCCCGGCTGCCGCTCCGCTATCCCGAGCGGCGTGGGCGAC 120
QY 482 CGGGCCCGAGCGGCGATCGTGCCTTTTCCCTTGGGAGTAGGATGTGTAAGGA 541
DB 121 CGGGCCCGAGCGGCGATCGTGCCTTTTCCCTTGGGAGTAGGATGTGTAAGGA 180
QY 542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAATCCGTAAGTGTCTGCGC 601
DB 181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAATCCGTAAGTGTCTGCGC 240
QY 602 TGGCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGCGATT 661

Sequence 107, Application US/10063551
 Publication No. US20020183494A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,551
 PRIORITY FILING DATE: 2002-05-02
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 107
 LENGTH: 2397
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-063-551-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	362	AGAGAAAGAGGCTCTCAGCTGAAGCAATGCGAGCCCTCCGGCTCTCCGCGAAGAGTT	421
DB	1	AGAGAAAGAGGCTCTCAGCTGAAGCAATGCGAGCCCTCCGGCTCTCCGCGAAGAGTT	60
QY	422	CCCTGCCCGATGAGCCCGCCGCGTGCCTCCCGACATCCCAAGGCGGGGCGGCGAC	481
DB	61	CCCTGCCCGATGAGCCCGCCGCGTGCCTCCCGACATCCCAAGGCGGGGCGGCGAC	120
QY	482	CGGGCCGAGCGCGAGATCGTGCCTGTTTCCCTTGGAGTAGGATGTTGGTGAAGGA	541
DB	121	CGGGCCGAGCGCGAGATCGTGCCTGTTTCCCTTGGAGTAGGATGTTGGTGAAGGA	180
QY	542	TGGGGCTTCTCCCTTACCGGGCTCACAATGCCAGAGAGATCCGTGAAGTGTCTGCGC	601
DB	181	TGGGGCTTCTCCCTTACCGGGCTCACAATGCCAGAGAGATCCGTGAAGTGTCTGCGC	240
QY	602	TGCTGTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAATGTGTGGCAGTT	661
DB	241	TGCTGTCTAGCGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAATGTGTGGCAGTT	300
QY	662	TCTGTCTGATGAGGAGTACTTAATAATGTTCTCACTTTAACTGACAGAAACGAGGTA	721
DB	301	TCTGTCTGATGAGGAGTACTTAATAATGTTCTCACTTTAACTGACAGAAACGAGGTA	360
QY	722	GAGGAGCAGTCAATTTGACTTACTTCTCTGTTTCAATCGGTCAATGTTGTTTGC	781
DB	361	GAGGAGCAGTCAATTTGACTTACTTCTCTGTTTCAATCGGTCAATGTTGTTTGC	420
QY	782	TGTTTCTTATCATTTGCGGATGTAGGATATTTGCGAATGCGGTAAGAAATCTGTTG	841
DB	421	TGTTTCTTATCATTTGCGGATGTAGGATATTTGCGAATGCGGTAAGAAATCTGTTG	480
QY	842	CTTCTGTGATGTTTGGAGTTTGTCTGCTCAATTTCTGTGAGAACTGGCTTGTGC	901
DB	481	CTTCTGTGATGTTTGGAGTTTGTCTGCTCAATTTCTGTGAGAACTGGCTTGTGC	540
QY	902	GTTTGGACATGACAGGACTTATGTTTCCGCTGACATGAGTGGTCAATGTTGCTTTC	961
DB	541	GTTTGGACATGACAGGACTTATGTTTCCGCTGACATGAGTGGTCAATGTTGCTTTC	600
QY	962	AAAGCAGGATGACAAATTTAGGATTAACCTAGATATCGGTGGCTTACTCATGTTGGAAT	1021
DB	601	AAAGCAGGATGACAAATTTAGGATTAACCTAGATATCGGTGGCTTACTCATGTTGGAAT	660

QY	1022	TTTTTTTTCAGAGAGATTTAAGTGTGTGGAGTAGTATATTTCACTGACTGTTGGAATG	1081
DB	661	TTTTTTTTCAGAGAGATTTAAGTGTGTGGAGTAGTATATTTCACTGACTGTTGGAATG	720
QY	1082	ACAGAGATGGACTGGCCCCCAGATTCTCTGCTGTGTAGAGAAATCCAGAGATGTTCCAAA	1141
DB	721	ACAGAGATGGACTGGCCCCCAGATTCTCTGCTGTGTAGAGAAATCCAGAGATGTTCCAAA	780
QY	1142	CAGGCCCCCAGAGAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAGAAATGAT	1201
DB	781	CAGGCCCCCAGAGAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAGAAATGAT	840
QY	1202	TCCTTTTTCAGAGAGAAACCAACCACTGCTGAGGTCTGAGTTTCTGGGAAATCTCCATGGG	1261
DB	841	TCCTTTTTCAGAGAGAAACCAACCACTGCTGAGGTCTGAGTTTCTGGGAAATCTCCATGGG	900
QY	1262	GTGACACAAATCCTGGCCCATGATCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT	1321
DB	901	GTGACACAAATCCTGGCCCATGATCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT	960
QY	1322	AGAGGGAGCTGGGGAGACACCAATGATGCTTTGAAGATGACAACTCTCAGCACCTG	1381
DB	961	AGAGGGAGCTGGGGAGACACCAATGATGCTTTGAAGATGACAACTCTCAGCACCTG	1020
QY	1382	TCATCTCCTCAGTAGAACTCTTGAACCAAGCCTGTCAAGAAATCTTTGAACACACATCC	1441
DB	1021	TCATCTCCTCAGTAGAACTCTTGAACCAAGCCTGTCAAGAAATCTTTGAACACACATCC	1080
QY	1442	ATGGCAAAACAGCTTTAATACACACTTTGAGATGAGGAGTTATAAAGAAATGTCACAG	1501
DB	1081	ATGGCAAAACAGCTTTAATACACACTTTGAGATGAGGAGTTATAAAGAAATGTCACAG	1140
QY	1502	AAGAAACCAACAACTTGTCTTACTGCACTTGTGAATTTTGTAGTACATATGTTGTTT	1561
DB	1141	AAGAAACCAACAACTTGTCTTACTGCACTTGTGAATTTTGTAGTACATATGTTGTTT	1200
QY	1562	CAGAAATGTAGAAATATAAATGTTGCCATAAATAACACCTTAAGCATATCTATCTTA	1621
DB	1201	CAGAAATGTAGAAATATAAATGTTGCCATAAATAACACCTTAAGCATATCTATCTTA	1260
QY	1622	TGCTTTAAATGAGATGGAAGTTTCATGTATAAGTCAACCACTGGACAAATAATGA	1681
DB	1261	TGCTTTAAATGAGATGGAAGTTTCATGTATAAGTCAACCACTGGACAAATAATGA	1320
QY	1682	TGCCCTTAAATGCTGAAGACAGATGTATACCCATGCTGTAGCTGTGTATGACTTTTA	1741
DB	1321	TGCCCTTAAATGCTGAAGACAGATGTATACCCATGCTGTAGCTGTGTATGACTTTTA	1380
QY	1742	CTGACACAGTATATGTTTGGAGGAGCATGTATAGTATGCTTCCGCAATCCATGCAAA	1801
DB	1381	CTGACACAGTATATGTTTGGAGGAGCATGTATAGTATGCTTCCGCAATCCATGCAAA	1440
QY	1802	CGAGTCACATATGTTGGGAGCTGGAGCCATAGTAAAGTTGATTTACTTCTACCAACTAGT	1861
DB	1441	CGAGTCACATATGTTGGGAGCTGGAGCCATAGTAAAGTTGATTTACTTCTACCAACTAGT	1500
QY	1862	ATATAAGTACTAATAAATGCTAAATAGAGAGTTAGAAAATTAATAAATCTTATTA	1921
DB	1501	ATATAAGTACTAATAAATGCTAAATAGAGAGTTAGAAAATTAATAAATCTTATTA	1560
QY	1922	CTCAGGATCTATTCTTCTGATGCTAAATAATATATATATATATATATATATATATAT	1981
DB	1561	CTCAGGATCTATTCTTCTGATGCTAAATAATATATATATATATATATATATATATAT	1620
QY	1982	TGACTTACCTAAATCTGATTTTGTGCTTACTAAATATCTTACCACTTAAAGAGCAA	2041
DB	1621	TGACTTACCTAAATCTGATTTTGTGCTTACTAAATATCTTACCACTTAAAGAGCAA	1680
QY	2042	GCTAACCATTTGCTTAAAGCTGATCAGGATTTTGTATATATATATATATATATATAT	2101
DB	1681	GCTAACCATTTGCTTAAAGCTGATCAGGATTTTGTATATATATATATATATATATAT	1740
QY	2102	TATATTCAGTCGATTTTCTGATTAATGTTTGAAGATTAACCATATATGAAGAGAAAT	2161

Db 1741 TATATTCAGTCGATTTTCAGTCTCTGATAATGTTAAGAAATACCCATTATGAAGAGGAAAT 1800
Qy 2162 TTGTCCTGTATAGCATCATTTATTTTAGCCCTTTCCTGTTAATAAGCTTTACTATTCTGT 2221
Db 1801 TTGTCCTGTATAGCATCATTTATTTTAGCCCTTTCCTGTTAATAAGCTTTACTATTCTGT 1860
Qy 2222 CCTGGCTTATATACATATAAATCTGTTATTAATACTAACCACCAATTTTGAAAAT 2281
Db 1861 CCTGGCTTATATACATATAAATCTGTTATTAATACTAACCACCAATTTTGAAAAT 1920
Qy 2282 TACCAGTGTATACATATAGGATCAATTTAGATGAGTCTGCTTTAGGAAGTATTA 2341
Db 1921 TACCAGTGTATACATATAGGATCAATTTAGATGAGTCTGCTTTAGGAAGTATTA 1980
Qy 2342 ATAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTCTCC 2401
Db 1981 ATAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTCTCC 2040
Qy 2402 CAATGAGACTCTTTTTCACACTAAACACTTTTAAAAAGCTTATCTTGCCCTTCTCCA 2461
Db 2041 CAATGAGACTCTTTTTCACACTAAACACTTTTAAAAAGCTTATCTTGCCCTTCTCCA 2100
Qy 2462 AACAGAAGCAATAGTCTCCAACTCAATATAAATTCACAGAAATAGTGTCTTTTCT 2521
Db 2101 AACAGAAGCAATAGTCTCCAACTCAATATAAATTCACAGAAATAGTGTCTTTTCT 2160
Qy 2522 CCAGAAAATGCTTGTAGAAATCATTTAAACATGTGACATTTAGAGATCTTTGTTTA 2581
Db 2161 CCAGAAAATGCTTGTAGAAATCATTTAAACATGTGACATTTAGAGATCTTTGTTTA 2220
Qy 2582 TTTCACTGATTAATATATCTGTGCAAAATACACAGATTTAATAATTTTTTACAGAGTA 2641
Db 2221 TTTCACTGATTAATATATCTGTGCAAAATACACAGATTTAATAATTTTTTACAGAGTA 2280
Qy 2642 TAGTATTTATTTGAAATGGGAAAGTGCAATTTACTGATTTTCTGATTTGTTAT 2701
Db 2281 TAGTATTTATTTGAAATGGGAAAGTGCAATTTACTGATTTTCTGATTTGTTAT 2340
Qy 2702 TTCTCAGATATGGAAGAAATTAATAATGTGCAATTAATTTTCTAGAGATAA 2758
Db 2341 TTCTCAGATATGGAAGAAATTAATAATGTGCAATTAATTTTCTAGAGATAA 2397

RESULT 15
US-10-174-581-323
; Sequence 323, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Fan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Query Match      86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 362 AGAGAAAGAAAGCGCTCCAGCTGAAGCAATGACGCCCTCCGGCTCTCGCGAAGATT 421
Db 1 AGAGAAAGAAAGCGCTCCAGCTGAAGCAATGACGCCCTCCGGCTCTCGCGAAGATT 60

QY 422 CCCTGCCCGATGAGCCCGCCGCGTCCCGACTATCCCGAGCGCGGCTGGGGCAC 481
Db 61 CCCTGCCCGATGAGCCCGCCGCGTCCCGACTATCCCGAGCGCGGCTGGGGCAC 120

QY 482 CGGGCCCGAGCGCGAGATCGCTGCGGTTTCCCTTGGAGTAGAGTGTGTGAAGGA 541
Db 121 CGGGCCCGAGCGCGAGATCGCTGCGGTTTCCCTTGGAGTAGAGTGTGTGAAGGA 180

QY 542 TGGGGCTTCTCCCTTACGGGGCTCACATGGCCGAGAGATCCCGTGAAGTGTCTGCC 601
Db 181 TGGGGCTTCTCCCTTACGGGGCTCACATGGCCGAGAGATCCCGTGAAGTGTCTGCC 240

QY 602 TGCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAAATGCCATCAGTGTGTGGCAGTT 661
Db 241 TGCTGCTCTAGCGCCCTCAATCTGCTCTTTTGGTTAAATGCCATCAGTGTGTGGCAGTT 300

QY 662 TCTGTTGGATGAGGACTACCTAAATAGTTTCTACCTTTAACTGCAGAAACGAGGTA 721
Db 301 TCTGTTGGATGAGGACTACCTAAATAGTTTCTACCTTTAACTGCAGAAACGAGGTA 360

QY 722 GAGGAGCAGTCAATTTGACTTCTCTGTTGTTTCTCCGGTCAATGTTGTTTTC 781
Db 361 GAGGAGCAGTCAATTTGACTTCTCTGTTGTTTCTCCGGTCAATGTTGTTTTC 420

QY 782 TGTTCCTTATCATTTGTTGGGATTTAGGATATTTGGAAACCGTGAAGAAATCTGTTG 841
Db 421 TGTTCCTTATCATTTGTTGGGATTTAGGATATTTGGAAACCGTGAAGAAATCTGTTG 480

QY 842 CTTCTTGATGTTGACTTTTGGAGTTTCTGTTGTTTCTGTTGTTGTTGTTGTTGTTG 901
Db 481 CTTCTTGATGTTGACTTTTGGAGTTTCTGTTGTTTCTGTTGTTGTTGTTGTTGTTG 540

QY 902 GTTTGGACATATGAACAGGAACCTATGTTTCCAGTACAATGGTTCAGATATGTTG 961
Db 541 GTTTGGACATATGAACAGGAACCTATGTTTCCAGTACAATGGTTCAGATATGTTG 600

QY 962 AAAGCCAGGATGACAAATTAATGATTACCTAGATATCGGTGGCTTACTCATGCTTGAAT 1021
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Db 601 AAAGCAGGATGACAAATATATGATACCTAGATATCGTGGCTTACTCATGCTTGGAAAT 660
Qy 1022 TTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTACTATATTTCACTGACTGGTGGAAATG 1081
Db 661 TTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTACTATATTTCACTGACTGGTGGAAATG 720
Qy 1082 ACAGAGATGAGTCTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCCAAGATGTCCTCAA 1141
Db 721 ACAGAGATGAGTCTGGCCCCCAGATTCCTGCTGTGTAGAGAAATCCCAAGATGTCCTCAA 780
Qy 1142 CAGGCCACAGGAGATCTCAGTGACCTTTATCAAGAGGGTGTGGAGAGAAATGATAT 1201
Db 781 CAGGCCACAGGAGATCTCAGTGACCTTTATCAAGAGGGTGTGGAGAGAAATGATAT 840
Qy 1202 TCCTTTTGTAGAGAAACCAACAACTGCAGGTCTGAGGTTCCTGGGAACTCTCCATTTGG 1261
Db 841 TCCTTTTGTAGAGAAACCAACAACTGCAGGTCTGAGGTTCCTGGGAACTCTCCATTTGG 900
Qy 1262 GTGACAAATCTCTGGCCATGATTTCTCACTATCTCTGCTGTGGGCTCTGTATATGAT 1321
Db 901 GTGACAAATCTCTGGCCATGATTTCTCACTATCTCTGCTGTGGGCTCTGTATATGAT 960
Qy 1322 AGAAGGAGCGGGGACAGACAAATGATGTCCTTGAAGAAATGACAACTCTCAGCACCTG 1381
Db 961 AGAAGGAGCGGGGACAGACAAATGATGTCCTTGAAGAAATGACAACTCTCAGCACCTG 1020
Qy 1382 TCATGTCCTCTCAGTGAACCTTTGAAACCAAGCTGTCAAGAAATCTTTGAACACATCC 1441
Db 1021 TCATGTCCTCTCAGTGAACCTTTGAAACCAAGCTGTCAAGAAATCTTTGAACACATCC 1080
Qy 1442 ATGGCAACAGCTTTATACACATTTGAGATGGAGAGTTATAAAGAAATGTCACAG 1501
Db 1081 ATGGCAACAGCTTTATACACATTTGAGATGGAGAGTTATAAAGAAATGTCACAG 1140
Qy 1502 AAGAAAAACCAACTTTTACTGACTTTGTGAATTTTGTAGTACATACTATGTGTTT 1561
Db 1141 AAGAAAAACCAACTTTTACTGACTTTGTGAATTTTGTAGTACATACTATGTGTTT 1200
Qy 1562 CAGAAATATGAGAAATATAAATTTGTCCTATAAATAACACCTTAAGCATATCTATCTTA 1621
Db 1201 CAGAAATATGAGAAATATAAATTTGTCCTATAAATAACACCTTAAGCATATCTATCTTA 1260
Qy 1622 TGCTTTAAATGAGATGGAAAGTTTCATGTCATAGTCAACCTGAGCAATATTTCA 1681
Db 1261 TGCTTTAAATGAGATGGAAAGTTTCATGTCATAGTCAACCTGAGCAATATTTCA 1320
Qy 1682 TGCCCTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTATGACTTTTA 1741
Db 1321 TGCCCTTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCTGTGTATGACTTTTA 1380
Qy 1742 CTGAACACAGTTATGTTTTCAGGACAGATGTTTGTAGTATGAGTTCCTGATCCATGCA 1801
Db 1381 CTGAACACAGTTATGTTTTCAGGACAGATGTTTGTAGTATGAGTTCCTGATCCATGCA 1440
Qy 1802 CGAGTCACATATGCTGGGCTGGAGCCATAGTAAAGGTTGATTTACTTCTACCACTAGT 1861
Db 1441 CGAGTCACATATGCTGGGCTGGAGCCATAGTAAAGGTTGATTTACTTCTACCACTAGT 1500
Qy 1862 ATATAAGTACTAATAAATGCTAATAGGAGTTAGAAATACTAATACTTTTATTA 1921
Db 1501 ATATAAGTACTAATAAATGCTAATAGGAGTTAGAAATACTAATACTTTTATTA 1560
Qy 1922 CTCAGGATCTATCTCTGATGCTAAATAATATATATATATATATATATATATATATAT 1981
Db 1561 CTCAGGATCTATCTCTGATGCTAAATAATATATATATATATATATATATATATATAT 1620
Qy 1982 TGACTACCTAATGCTGATTTTGTCTGTTACTAATAATATCTTACCACTTAAAGAGCAA 2041
Db 1621 TGACTACCTAATGCTGATTTTGTCTGTTACTAATAATATCTTACCACTTAAAGAGCAA 1680
Qy 2042 GCTTAAACACATTTGCTTAAAGTCTGATCAGGATTTTGTATATATATATATATATATAT 2101

Db 1681 GCTTAAACACATTTGCTTAAAGTCTGATCAGGATTTTGTATATATATATATATATAT 1740
Qy 2102 TATATATCAGTCTGATTTCTGATATCTGATATCTGATATCTGATATCTGATATCTGAT 2161
Db 1741 TATATATCAGTCTGATTTCTGATATCTGATATCTGATATCTGATATCTGATATCTGAT 1800
Qy 2162 TTGCTCTGTATAGCATCATTTATTTTAGCCTTTCTGTTAATAAAGCTTTACTATCTGT 2221
Db 1801 TTGCTCTGTATAGCATCATTTATTTTAGCCTTTCTGTTAATAAAGCTTTACTATCTGT 1860
Qy 2222 CTTGGGCTTTATATACATATACATATCTGTTATTTAATACTTTAAACCTTTTGA 2281
Db 1861 CTTGGGCTTTATATACATATACATATCTGTTATTTAATACTTTAAACCTTTTGA 1920
Qy 2282 TACCAGTGTATACATAGGAATCATTTTCAAGATGTAGTCTGCTTTTAGAAGTATTA 2341
Db 1921 TACCAGTGTATACATAGGAATCATTTTCAAGATGTAGTCTGCTTTTAGAAGTATTA 1980
Qy 2342 ATAGAAATTTTGCATATACCTTAGTTCATTCAGAAAGGACTTTGATGCTGTTTTCTCC 2401
Db 1981 ATAGAAATTTTGCATATACCTTAGTTCATTCAGAAAGGACTTTGATGCTGTTTTCTCC 2040
Qy 2402 CAAATGAAGACTCTTTTTCAGACTTAAACACACTTTTAAAGCTTATCTTTGCCCTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTTCAGACTTAAACACACTTTTAAAGCTTATCTTTGCCCTCTCCA 2100
Qy 2462 AACAAAGAGCAATAGTCTCCAAGTCAATATATAATTTTACAGAAATAGTGTCTTTTTCT 2521
Db 2101 AACAAAGAGCAATAGTCTCCAAGTCAATATATAATTTTACAGAAATAGTGTCTTTTTCT 2160
Qy 2522 CCAGAAATGCTTGTGAGAAATCAATTAACATGTCAGAAATTTAGAGATCTTTGTTTTA 2581
Db 2161 CCAGAAATGCTTGTGAGAAATCAATTAACATGTCAGAAATTTAGAGATCTTTGTTTTA 2220
Qy 2582 TTTTCACTGATTAATATACTGTGGCAATTTACAGATTTATAATTTTACAGAGTA 2641
Db 2221 TTTTCACTGATTAATATACTGTGGCAATTTACAGATTTATAATTTTACAGAGTA 2280
Qy 2642 TAGTATATTTTGAATGGGAAAGTGCATTTTACTGTTATTTGTGTTATTTGTTTTAT 2701
Db 2281 TAGTATATTTTGAATGGGAAAGTGCATTTTACTGTTATTTGTGTTATTTGTTTTAT 2340
Qy 2702 TTCTCAGAAATGGAAGAAATTTAAATGTCATTAATATTTTCTAGAGAGTAA 2758
Db 2341 TTCTCAGAAATGGAAGAAATTTAAATGTCATTAATATTTTCTAGAGAGTAA 2397

Search completed: May 17, 2004, 20:29:31
Job time : 1155.36 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 01:41:21 ; Search time 1058.17 Seconds
(without alignments)
11112.549 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tgaagccaccattttaag.....tagagagtaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2768	100.0	2768	3 AAA27100	Aaa27100 CDNA enco
2	2393.8	86.5	2397	3 AAA37098	Aaa37098 Human PRO
3	2393.8	86.5	2397	4 AAF54395	Aaf54395 DNA enco
4	2393.8	86.5	2397	4 AAS46086	Aas46086 Human DNA
5	2393.8	86.5	2397	4 AAF92111	Aaf92111 Human PRO
6	2393.8	86.5	2397	6 ABS74431	AbS74431 Human CDN
7	2393.8	86.5	2397	7 AEX78689	AbX78689 Human PRO
8	2393.8	86.5	2397	7 ACA75661	Aca75661 Novel hum
9	2393.8	86.5	2397	7 ACA71141	Aca71141 Human sec
10	2393.8	86.5	2397	7 ACC87669	Acc87669 Human sec
11	2393.8	86.5	2397	7 ACC87055	Acc87055 Human sec
12	2393.8	86.5	2397	7 ACD04228	Acd04228 Human sec
13	2393.8	86.5	2397	7 ACA69559	Aca69559 CDNA enco
14	2393.8	86.5	2397	7 ACA90404	Aca90404 Novel hum
15	2393.8	86.5	2397	7 ACC89511	Acc89511 Human sec
16	2393.8	86.5	2397	7 ACA98302	Aca98302 Novel hum
17	2393.8	86.5	2397	7 ACA93944	Aca93944 Human sec
18	2393.8	86.5	2397	7 ACD15337	Acd15337 Human sec
19	2393.8	86.5	2397	7 ACD08924	Acd08924 Human sec
20	2393.8	86.5	2397	7 ACC96844	Acc96844 Human sec
21	2393.8	86.5	2397	7 ACF15565	Acf15565 Human sec
22	2393.8	86.5	2397	7 ACA72932	Aca72932 Human PRO
23	2393.8	86.5	2397	7 ACD03104	Acd03104 Novel hum

24	2393.8	86.5	2397	7 ACD01919	Acd01919 Novel hum
25	2393.8	86.5	2397	7 ACA92111	Aca92111 Novel hum
26	2393.8	86.5	2397	7 ACA89536	Aca89536 CDNA enco
27	2393.8	86.5	2397	7 ACA73546	Aca73546 Human sec
28	2393.8	86.5	2397	7 ACA05861	Aca05861 Human sec
29	2393.8	86.5	2397	7 ACA66695	Aca66695 CDNA enco
30	2393.8	86.5	2397	7 ACA91217	Aca91217 Novel hum
31	2393.8	86.5	2397	7 ACD81594	Acd81594 Human CDN
32	2393.8	86.5	2397	7 ACF20270	Acf20270 Human sec
33	2393.8	86.5	2397	7 ACF19656	Acf19656 Human sec
34	2393.8	86.5	2397	7 ACD21944	Acd21944 Human sec
35	2393.8	86.5	2397	7 ACF13109	Acf13109 Human sec
36	2393.8	86.5	2397	7 ACD25212	Acd25212 Human sec
37	2393.8	86.5	2397	7 ACF00261	Acf00261 Human sec
38	2393.8	86.5	2397	7 ACA60416	Aca60416 Novel hum
39	2393.8	86.5	2397	7 ACA72318	Aca72318 Novel hum
40	2393.8	86.5	2397	7 ACD04842	Acd04842 Novel hum
41	2393.8	86.5	2397	7 ACD18303	Acd18303 Human sec
42	2393.8	86.5	2397	7 ACD08310	Acd08310 Human sec
43	2393.8	86.5	2397	7 ACA88744	Aca88744 Novel hum
44	2393.8	86.5	2397	7 ACA70186	Aca70186 Human sec
45	2393.8	86.5	2397	7 ACD12408	Acd12408 Novel hum

ALIGNMENTS

RESULT 1
AAA27100
ID AAA27100 standard; CDNA; 2768 BP.
XX
AC AAA27100;
XX
DT 28-JUL-2000 (first entry)
XX
DE cDNA encoding human TM4P-2.
XX
KW Human; transmembrane 4 protein; TM4P; tetraspan; cancer;
KW developmental disorder; cell proliferation disorder;
KW immunological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT 569..1486
FT /*tag= a
FT /product= "TM4P-2"
XX
PN WO200026243-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025499.
XX
PR 29-OCT-1998; 98US-0172249P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Argentine CC, Corley NC, Gorgone GA, Guegler KJ;
PI Baughn MR;
XX
DR WPI; 2000-376122/32.
DR P-PSDB; AAY94420.
XX
PT Human transmembrane 4 proteins (TM4P) useful for diagnosis, treatment and
PT prevention of disorders associated with expression of TM4P such as
XX developmental disorders.
XX
PS Claim 9; Fig 2; 86pp; English.
XX
CC Human transmembrane 4 protein (TM4P) is involved in development,
CC inflammation and cell proliferation. The protein acts through signal
transduction, control of cell adhesion and regulation of cell growth. A

CC pharmaceutical composition of TM4P could be used to treat a condition
 CC associated with disrupted expression of TM4P, such as immunological,
 CC developmental and cell proliferation disorders. In addition antibodies
 CC which specifically bind TM4P may be used for the diagnosis of disorders
 CC characterised by expression of TM4P. The present sequence is the cDNA
 CC encoding human TM4P-2 from Incyte Clone 2674553. This clone was derived
 CC from kidney tissue cDNA library KIDNOR19
 XX

SQ Sequence 2768 BP; 789 A; 530 C; 607 G; 842 T; 0 U; 0 Other;

Query Match 100.0%; Score 2768; DB 3; Length 2768;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCGACGCCACCAATTTAAAGGGATTACTCAGCGACTTCCCAAGTTCCTAGGCATTA	60
Db	1	TCGACGCCACCAATTTAAAGGGATTACTCAGCGACTTCCCAAGTTCCTAGGCATTA	60
Qy	61	TCCTCTGGACCTATCTCGAGAGTGAAGGTCCTTTGGGACTCTCGCTGGTGAGA	120
Db	61	TCCTCTGGACCTATCTCGAGAGTGAAGGTCCTTTGGGACTCTCGCTGGTGAGA	120
Qy	121	GGGCAAGAAACACCCACTAGGACCCCAACCCCGGACGCCGCTCGAGCATGCGCTGA	180
Db	121	GGGCAAGAAACACCCACTAGGACCCCAACCCCGGACGCCGCTCGAGCATGCGCTGA	180
Qy	181	GAGTTTGTGAGCTGGCCCTGGCTGCGCGCTGCTCTGCGGACTCGGAGAGACTTG	240
Db	181	GAGTTTGTGAGCTGGCCCTGGCTGCGCGCTGCTCTGCGGACTCGGAGAGACTTG	240
Qy	241	GGAGGACAGCGGCGCTGGGAGTGGCTTAGCAGAGACTTTCCAGAACTGCTGCCACG	300
Db	241	GGAGGACAGCGGCGCTGGGAGTGGCTTAGCAGAGACTTTCCAGAACTGCTGCCACG	300
Qy	301	ACTTTTCTTTTCTTTTCTTTTCCAGAGCGCGGAGCGCGCGCGGGGGGAGAGG	360
Db	301	ACTTTTCTTTTCTTTTCTTTTCCAGAGCGCGGAGCGCGCGCGGGGGGAGAGG	360
Qy	361	AAGAGAAAGAGCTCTCCAGCTGAGCCAAATCAGCCCTCCGGCTCTCCGCGAAGAT	420
Db	361	AAGAGAAAGAGCTCTCCAGCTGAGCCAAATCAGCCCTCCGGCTCTCCGCGAAGAT	420
Qy	421	TCCTGCCCCGATCAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGGGCTGGGGCA	480
Db	421	TCCTGCCCCGATCAGCCCCCGCGTGGTCCCGACTATCCCGAGCGGGGCTGGGGCA	480
Qy	481	CCGGCCCCCAGCGGAGATCGTGGCTGGTTTCCCTTGGAGTAGGATGTGGTGAAGG	540
Db	481	CCGGCCCCCAGCGGAGATCGTGGCTGGTTTCCCTTGGAGTAGGATGTGGTGAAGG	540
Qy	541	ATGGGGCTTCTCCCTTACGGGGCTCAATGGGCAGAGAAGATTCCGTGAAGTGTCTGG	600
Db	541	ATGGGGCTTCTCCCTTACGGGGCTCAATGGGCAGAGAAGATTCCGTGAAGTGTCTGG	600
Qy	601	CTGCTGCTCAGCCCTCAATCTGCTTTTGGTTAATGTCCATCAGTGTGTGCGAGT	660
Db	601	CTGCTGCTCAGCCCTCAATCTGCTTTTGGTTAATGTCCATCAGTGTGTGCGAGT	660
Qy	661	TTCTGCTTGGATCAGGACTACCTAAATATGTTCTCACTTTAACTGCGAGAACGAGGT	720
Db	661	TTCTGCTTGGATCAGGACTACCTAAATATGTTCTCACTTTAACTGCGAGAACGAGGT	720
Qy	721	AGAGGAAGCAGTCATTTCGCTTCTCTGTTGTTTCCGGTTCATGTTGCTGTTTG	780
Db	721	AGAGGAAGCAGTCATTTCGCTTCTCTGTTGTTTCCGGTTCATGTTGCTGTTTG	780
Qy	781	CTGTTTCTTATCATTTGGGGATGTAGGATATCTGGAACGGTCAAGAAATCTGTT	840
Db	781	CTGTTTCTTATCATTTGGGGATGTAGGATATCTGGAACGGTCAAGAAATCTGTT	840
Qy	841	GCTTCTTGATGTTGGAAGTTGCTTGTCAITTTCTGTGTAGAACITGGCTTGGG	900
Db	841	GCTTCTTGATGTTGGAAGTTGCTTGTCAITTTCTGTGTAGAACITGGCTTGGG	900

Qy	901	CGTTTGGACATATGAACAGGAACCTTATGTTTCCAGTCAATGGTCAGATATGGTCACTTT	960
Db	901	CGTTTGGACATATGAACAGGAACCTTATGTTTCCAGTCAATGGTCAGATATGGTCACTTT	960
Qy	961	GAAAGCCAGGATGACAAATATGATGATACCTAGATATCGGTGGCTTACTCATGCTGAA	1020
Db	961	GAAAGCCAGGATGACAAATATGATGATACCTAGATATCGGTGGCTTACTCATGCTGAA	1020
Qy	1021	TTTTTTTTCAGAGAGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACTGTTGGAAT	1080
Db	1021	TTTTTTTTCAGAGAGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACTGTTGGAAT	1080
Qy	1081	GACAGAGATGCACTGGCCCCCAGATCTCTGCTGTGTGTAGAGAATTTCCAGAGATGTTCAA	1140
Db	1081	GACAGAGATGCACTGGCCCCCAGATCTCTGCTGTGTGTAGAGAATTTCCAGAGATGTTCAA	1140
Qy	1141	ACAGGCCACACAGGAGATCTCAGTGACCTTTATCAAGAGGTTTGTGGGAAGAAATGTA	1200
Db	1141	ACAGGCCACACAGGAGATCTCAGTGACCTTTATCAAGAGGTTTGTGGGAAGAAATGTA	1200
Qy	1201	TTCCCTTTTGGAGAGAACCAAAACAACTGAGGCTGCTGAGGTTTCTGGGAATCTCCATTG	1260
Db	1201	TTCCCTTTTGGAGAGAACCAAAACAACTGAGGCTGCTGAGGTTTCTGGGAATCTCCATTG	1260
Qy	1261	GGTGACAAATCTTGGCCATGATTTCTCATTACTCTGCTCTGGGCTCTGTATTATGA	1320
Db	1261	GGTGACAAATCTTGGCCATGATTTCTCATTACTCTGCTCTGGGCTCTGTATTATGA	1320
Qy	1321	TAGAAGGAGCGGGGACAGACCAAAATGATGCTCTTGAAGAAATGACAACTCTCAGCACCT	1380
Db	1321	TAGAAGGAGCGGGGACAGACCAAAATGATGCTCTTGAAGAAATGACAACTCTCAGCACCT	1380
Qy	1381	GTCAATGTCCTCAGTAGAATCTTTGAAACCAAGCTGTCAAGAACTTTTGAACACATC	1440
Db	1381	GTCAATGTCCTCAGTAGAATCTTTGAAACCAAGCTGTCAAGAACTTTTGAACACATC	1440
Qy	1441	CATGCAAAACAGCTTTAATACACACTTTGAGATGGAGGATTAATAAAGAAATGTCA	1500
Db	1441	CATGCAAAACAGCTTTAATACACACTTTGAGATGGAGGATTAATAAAGAAATGTCA	1500
Qy	1501	GAGAAACCAACAACTTTTACTGGACTTGTGAAATTTTGGAGTACATCTATGTGTT	1560
Db	1501	GAGAAACCAACAACTTTTACTGGACTTGTGAAATTTTGGAGTACATCTATGTGTT	1560
Qy	1561	TCAGAAATATGAGAAATAAATTTGCCATTAATAAATTAACACCTAAGCATATCTATCT	1620
Db	1561	TCAGAAATATGAGAAATAAATTTGCCATTAATAAATTAACACCTAAGCATATCTATCT	1620
Qy	1621	ATGCTTTAAATAGGATGGAAGATTTTCAATCAATAGTCACCACTGAGCAATATTTG	1680
Db	1621	ATGCTTTAAATAGGATGGAAGATTTTCAATCAATAGTCACCACTGAGCAATATTTG	1680
Qy	1681	ATGCCCTTAAATGCTGAAGACAGATCTATACCACTGTGTAGCTGTGTATGACTTTT	1740
Db	1681	ATGCCCTTAAATGCTGAAGACAGATCTATACCACTGTGTAGCTGTGTATGACTTTT	1740
Qy	1741	ACTCAACACAGTTATGTTTTGAGCGAGCTGTTTGAATAGCATTTCCGCATCCATGCAA	1800
Db	1741	ACTCAACACAGTTATGTTTTGAGCGAGCTGTTTGAATAGCATTTCCGCATCCATGCAA	1800
Qy	1801	ACGAGTCACATATGTTGGGACCTGAGCCATAGTAAAGTTGATTTACTTCTCACTAG	1860
Db	1801	ACGAGTCACATATGTTGGGACCTGAGCCATAGTAAAGTTGATTTACTTCTCACTAG	1860
Qy	1861	TATATAAGTACTAATTAATGCTTACATAGGAGTTAGAAATCTAATACTTTTAT	1920
Db	1861	TATATAAGTACTAATTAATGCTTACATAGGAGTTAGAAATCTAATACTTTTAT	1920
Qy	1921	ACTCAGCGATCTATCTTCTGATGCTAAATTAATATATATCAGAAACCTTCAATATG	1980
Db	1921	ACTCAGCGATCTATCTTCTGATGCTAAATTAATATATATCAGAAACCTTCAATATG	1980

Qy	1981	GTGACTACCTAAATGTAATTTTGGTGGTGTCTTAAATAATTTCTTACCACCTTAAAGAGCA	2040	XX	09-MAR-2000.	
Db	1981	GTGACTACCTAAATGTAATTTTGGTGGTGTCTTAAATAATTTCTTACCACCTTAAAGAGCA	2040	XX	01-SEP-1999;	99WO-US020111.
Qy	2041	AGCTAACACATGCTTAAAGCTGATCAGGGAATTTTGTATATAAGTCTGTGTTAAATCT	2100	XX	01-SEP-1998;	98US-0098715P.
Db	2041	AGCTAACACATGCTTAAAGCTGATCAGGGAATTTTGTATATAAGTCTGTGTTAAATCT	2100	PR	01-SEP-1998;	98US-0098749P.
Qy	2101	GTATATTCCTAGTCGATTTGCTGATATGTAAGATAACCATTTATGAAAGGAAA	2160	PR	02-SEP-1998;	98US-0098803P.
Db	2101	GTATATTCCTAGTCGATTTGCTGATATGTAAGATAACCATTTATGAAAGGAAA	2160	PR	02-SEP-1998;	98US-0098821P.
Qy	2161	TTTGCTCTGTATAGCATTAATTTTAGCCTTTCCGTTTAAATAAGCTTACTATTCTG	2220	PR	02-SEP-1998;	98US-0098843P.
Db	2161	TTTGCTCTGTATAGCATTAATTTTAGCCTTTCCGTTTAAATAAGCTTACTATTCTG	2220	PR	09-SEP-1998;	98US-0099536P.
Qy	2221	TCCTGGGCTTATATTACACATATAACCTGTTTAAATAACTTAAACCACTAAATTTTGA	2280	PR	09-SEP-1998;	98US-0099596P.
Db	2221	TCCTGGGCTTATATTACACATATAACCTGTTTAAATAACTTAAACCACTAAATTTTGA	2280	PR	09-SEP-1998;	98US-0099598P.
Qy	2281	TTACCACTGTGATACATAGGAATCAATTTTTCAGATGTAGTCTGGCTTTTAGGAAGTAT	2340	PR	09-SEP-1998;	98US-0099602P.
Db	2281	TTACCACTGTGATACATAGGAATCAATTTTTCAGATGTAGTCTGGCTTTTAGGAAGTAT	2340	PR	09-SEP-1998;	98US-0099642P.
Qy	2341	AATAGAAAATTTGCAATTAACCTTAGTTGATTCAGAAAGGACTGTATGCTGTTTTCTC	2400	PR	10-SEP-1998;	98US-0099741P.
Db	2341	AATAGAAAATTTGCAATTAACCTTAGTTGATTCAGAAAGGACTGTATGCTGTTTTCTC	2400	PR	10-SEP-1998;	98US-0099754P.
Qy	2401	CCAAATCAAGACTCTTTTTCACACTAACTTTTAAAGAGCTTATCTTTGCTCTCTCC	2460	PR	10-SEP-1998;	98US-0099763P.
Db	2401	CCAAATCAAGACTCTTTTTCACACTAACTTTTAAAGAGCTTATCTTTGCTCTCTCC	2460	PR	10-SEP-1998;	98US-0099792P.
Qy	2461	AAACAAGAAAGCTTTTTCAGACTAACTTTTAAAGAGCTTATCTTTGCTCTCTCC	2520	PR	10-SEP-1998;	98US-0099808P.
Db	2461	AAACAAGAAAGCTTTTTCAGACTAACTTTTAAAGAGCTTATCTTTGCTCTCTCC	2520	PR	10-SEP-1998;	98US-0099812P.
Qy	2521	TCGAGAAAATGCTTTGAGAACTTAAACATGTACAGATTTAGAGATTTCTTTGTTT	2580	PR	10-SEP-1998;	98US-0099815P.
Db	2521	TCGAGAAAATGCTTTGAGAACTTAAACATGTACAGATTTAGAGATTTCTTTGTTT	2580	PR	10-SEP-1998;	98US-0099816P.
Qy	2581	ATTTCACTGATTAATATACCTGTCGCAATTTACACAGATTTAAATTTTTCACAGAGT	2640	PR	15-SEP-1998;	98US-0100385P.
Db	2581	ATTTCACTGATTAATATACCTGTCGCAATTTACACAGATTTAAATTTTTCACAGAGT	2640	PR	15-SEP-1998;	98US-0100388P.
Qy	2641	ATAGTATTTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTATTTGTTA	2700	PR	15-SEP-1998;	98US-0100390P.
Db	2641	ATAGTATTTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTATTTGTTA	2700	PR	16-SEP-1998;	98US-0100584P.
Qy	2701	TTTCTCAGATATGGAAGAAAATTTAAATGTGTCATTAATTTTCTAGAGAGTAAAA	2760	PR	16-SEP-1998;	98US-0100627P.
Db	2701	TTTCTCAGATATGGAAGAAAATTTAAATGTGTCATTAATTTTCTAGAGAGTAAAA	2760	PR	16-SEP-1998;	98US-0100661P.
Qy	2761	AAAAAAA 2768		PR	16-SEP-1998;	98US-0100662P.
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RESULT 2						98US-0100683P.
AAA37098						98US-0100684P.
ID	AAA37098 standard; cDNA; 2397 BP.					98US-0100710P.
XX						98US-0100711P.
AC	AAA37098;					98US-0100919P.
XX	08-AUG-2000 (first entry)					98US-0100930P.
DI	Human PRO1568, (UNQ774) cDNA sequence SEQ ID NO:272.					98US-0100848P.
DE	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;					98US-0101014P.
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.					98US-0101068P.
KW						98US-0101071P.
XX	Homo sapiens.					98US-0101279P.
OS						98US-0101471P.
XX	WO200012708-A2.					98US-0101472P.
FN						98US-0101473P.

PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
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 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
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 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX (GETH) GENENTECH INC.

XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 PI WPI; 2000-237871/20.
 XX P-PSDB; AAY99416.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT P80 polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 2; Fig 153; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted P80 polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor P80 proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences

CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;
 SQ

Query Match 86.5%; Score 2393.8; DB 3; Length 2397;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 362 AGAGAAAGAGCGTCTCCAGTGAAGCCATGACAGCCCTCCGGCTCTCCGGGAAGAGTT 421
 DB 1 AGAGAAAGAGCGTCTCCAGTGAAGCCATGACAGCCCTCCGGCTCTCCGGGAAGAGTT 60
 QY 422 CCCTGCCCGGATGAGCCCGCCGCGTGGTCCCGGACTATCCCGAGGCGGCGTGGGCAC 481
 DB 61 CCCTGCCCGGATGAGCCCGCCGCGTGGTCCCGGACTATCCCGAGGCGGCGTGGGCAC 120
 QY 482 CGGGCCAGCGCCGACGATCGTCCGCTTTTCCCTTGGGAGTAGGATGTCGTGAAAGGA 541
 DB 121 CGGGCCAGCGCCGACGATCGTCCGCTTTTCCCTTGGGAGTAGGATGTCGTGAAAGGA 180
 QY 542 TGGGGCTTCTCCCTTACGGGCTCACATGCGCAGAGAGATTCCGTGAAGTGTCTGGC 601
 DB 181 TGGGGCTTCTCCCTTACGGGCTCACATGCGCAGAGAGATTCCGTGAAGTGTCTGGC 240
 QY 602 TGCCTGCTTACGGCCCTCAATCTGCTCTTTTGGTAAATGTCCATCAGTGTGTGGCAGTT 661
 DB 241 TGCCTGCTTACGGCCCTCAATCTGCTCTTTTGGTAAATGTCCATCAGTGTGTGGCAGTT 300
 QY 662 TCTGCTTGGATGAGGACTACTAAATAAAGTTCTCACTTTAACTGAGAAACGAGGGA 721
 DB 301 TCTGCTTGGATGAGGACTACTAAATAAAGTTCTCACTTTAACTGAGAAACGAGGGA 360
 QY 722 GAGGAAGCAGTCATTTGACCTTCTCCGTCGTTTCATCGGTCATGATGCTGTTGTC 781
 DB 361 GAGGAAGCAGTCATTTGACCTTCTCCGTCGTTTCATCGGTCATGATGCTGTTGTC 420
 QY 782 TGTTTCTTATCATTGTGGGATCTTAGGATATTGTGGAACGCTGAAAGAAATCTCTTG 841
 DB 421 TGTTTCTTATCATTGTGGGATCTTAGGATATTGTGGAACGCTGAAAGAAATCTCTTG 480
 QY 842 CTCTTGCATGCTATTTGGAGTTGCTTGTCTATTTCTGTGTAGAACTGGCTTGGC 901
 DB 481 CTCTTGCATGCTATTTGGAGTTGCTTGTCTATTTCTGTGTAGAACTGGCTTGGC 540
 QY 902 GTTTGGACATATGAACAGGAACCTTATGTTTCCAGTACAATGGTCAGATATGTCACATTG 961
 DB 541 GTTTGGACATATGAACAGGAACCTTATGTTTCCAGTACAATGGTCAGATATGTCACATTG 600
 QY 962 AAAGCCAGGATGACAAATATGATGATACCTAGATATCGTGGCTTACTCATGCTTGAAT 1021
 DB 601 AAAGCCAGGATGACAAATATGATGATACCTAGATATCGTGGCTTACTCATGCTTGAAT 660
 QY 1022 TTTTTCAGAGAGAGTTTAAGTGTGTGGAGTAGTATATTTCAGTACTGTTGGAAATG 1081
 DB 661 TTTTTCAGAGAGAGTTTAAGTGTGTGGAGTAGTATATTTCAGTACTGTTGGAAATG 720
 QY 1082 ACAGAGATGAGACTGGCCCCCAGATTCCTGTGTGTAGAGAAATCCAGAGATGTTCCAAA 1141
 DB 721 ACAGAGATGAGACTGGCCCCCAGATTCCTGTGTGTAGAGAAATCCAGAGATGTTCCAAA 780
 QY 1142 CAGCCACACAGGAGATCTCAGTGACCTTATCAAGAGGTTGTGGGAGAGAAATGAT 1201
 DB 781 CAGCCACACAGGAGATCTCAGTGACCTTATCAAGAGGTTGTGGGAGAGAAATGAT 840
 QY 1202 TCTTTTTCAGAGAGAACCAAACTGAGTGTGTGGAGTTTCTGGGAATCTCCATTGG 1261
 DB 841 TCTTTTTCAGAGAGAACCAAACTGAGTGTGTGGAGTTTCTGGGAATCTCCATTGG 900
 QY 1262 GTGACAAATCTGGCCATGATCTCAGTACTTCTGCTGCTGGGCTGTATTATGAT 1321

901 GTGACACAAATCTGGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
1322 AGAAGGGAGCCGGGAGCAGACCAATGATGTCCTTTGAAGATGACAACTCTCAGCACCTG 1381
961 AGAAGGGAGCCCTGGGAGCAGACCAATGATGTCCTTTGAAGATGACAACTCTCAGCACCTG 1020
1382 TCATGTCCTCAGTAGAAGCTGTTGAACCAAGCCTGTCAGAACTCTTTGAGCAGACATCC 1441
1021 TCATGTCCTCAGTAGAAGCTGTTGAACCAAGCCTGTCAGAACTCTTTGAGCAGACATCC 1080
1442 ATGSCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATATAAAGAAATGTCTACAG 1501
1081 ATGSCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATATAAAGAAATGTCTACAG 1140
1502 AAGAAACCAACAACTGTTTACTGGACTGTGCAATTTTGGATACATACATCTGTTTT 1561
1441 AAGAAACCAACAACTGTTTACTGGACTGTGCAATTTTGGATACATACATCTGTTTT 1200
1562 CAGAAATATGTAGAAATATAAATGTTGCCATAAATAACCACTTAAGCATATACATTTCTA 1621
1201 CAGAAATATGTAGAAATATAAATGTTGCCATAAATAACCACTTAAGCATATACATTTCTA 1260
1622 TGCCTTTAAATGAGGATGGAAAGTTTCATGTCATTAAGTCACCACTTGGACATTAATGA 1681
1261 TGCCTTTAAATGAGGATGGAAAGTTTCATGTCATTAAGTCACCACTTGGACATTAATGA 1320
1682 TGCCTTTAAATGAGGATGGAAAGTTTCATGTCATTAAGTCACCACTTGGATGACTTTTA 1741
1321 TGCCTTTAAATGAGGATGGAAAGTTTCATGTCATTAAGTCACCACTTGGATGACTTTTA 1380
1742 CTGAACACAGTTATGTTTGGAGGAGCATGTTTGGATTAGCATTTCCGCACTCCATGCCAAA 1801
1381 CTGAACACAGTTATGTTTGGAGGAGCATGTTTGGATTAGCATTTCCGCACTCCATGCCAAA 1440
1802 CGAGTCATATGTTGGGAGCATGAGGAGCATGTTTGGATTAGCATTTCTACCACTAGT 1861
1441 CGAGTCATATGTTGGGAGCATGAGGAGCATGTTTGGATTAGCATTTCTACCACTAGT 1500
1862 ATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAATACTAATAACTTTTATTA 1921
1501 ATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAATACTAATAACTTTTATTA 1560
1922 CTCAGCATATCTTCTGATGCTAATAAATAAATATATATACAGAAACTTTCAATATGG 1981
1561 CTCAGCATATCTTCTGATGCTAATAAATAAATATATATACAGAAACTTTCAATATGG 1620
1982 TGACTACTAATGCTGATTTTGTGCTGTTACTAATAATATCTTACCACCTTTAAAGAGCAA 2041
1621 TGACTACTAATGCTGATTTTGTGCTGTTACTAATAATATCTTACCACCTTTAAAGAGCAA 1680
2042 GCTAACACATGCTTAAAGCTGATCAGGAGTTTCTTATATAAGTCTGTGTTAAATCTG 2101
1681 GCTAACACATGCTTAAAGCTGATCAGGAGTTTCTTATATAAGTCTGTGTTAAATCTG 1740
2102 TATAATTCAGTCGATTTTCAGTCTGATAATGTTAAGATACCACTTATGAAAGGAAAT 2161
1741 TATAATTCAGTCGATTTTCAGTCTGATAATGTTAAGATACCACTTATGAAAGGAAAT 1800
2162 TTGCTCTGTATAGCATCATTTATTTAGCCTTTCTCTGTTAATAAGCTTTACTATTCTGT 2221
1801 TTGCTCTGTATAGCATCATTTATTTAGCCTTTCTCTGTTAATAAGCTTTACTATTCTGT 1860
2222 CCTGGCTTATATACACATATACTGTTATTTAAATACCTTAACCACTAATTTTGAAT 2281
1861 CCTGGCTTATATACACATATACTGTTATTTAAATACCTTAACCACTAATTTTGAAT 1920
2282 TACCAGTGTGATACATAGGATCATTTATCAGATGTAGTCTGTTTAAAGGAGTATTA 2341
1921 TACCAGTGTGATACATAGGATCATTTATCAGATGTAGTCTGTTTAAAGGAGTATTA 1980
2342 ATAAGAAATTTGCATAAATTTAGTTGATTCAGAAAGAGCTTGTATGCTGTTTTTCTCC 2401
1981 ATAAGAAATTTGCATAAATTTAGTTGATTCAGAAAGAGCTTGTATGCTGTTTTTCTCC 2040

2402 CAAATGAGAGCTCTTTTTCACACTAAACACTTTTAAAAAGCTTATCTTTGCTTCTCCA 2461
2041 CAAATGAGAGCTCTTTTTCACACTAAACACTTTTAAAAAGCTTATCTTTGCTTCTCCA 2100
2462 AACAAGAACCAATAGTCTCCAGTCAATATAAATCTCAGAAATAGTGTCTTTTCT 2521
2101 AACAAGAACCAATAGTCTCCAGTCAATATAAATCTCAGAAATAGTGTCTTTTCT 2160
2522 CCAGAAAAATGCTTGTGAGAAATCATTTAAACATGTGACAAATTTAGAGATTTCTTTT 2581
2161 CCAGAAAAATGCTTGTGAGAAATCATTTAAACATGTGACAAATTTAGAGATTTCTTTT 2220
2582 TTTCCTGATTAATATACCTGTCGCAATTTACACAGATTTAAATTTTACAGAGTA 2641
2221 TTTCCTGATTAATATACCTGTCGCAATTTACACAGATTTAAATTTTACAGAGTA 2280
2642 TAGTATATTTTGAATGGAATGGGAAAGTGCATTTTACTGTATTTTGTGTTTAT 2701
2281 TAGTATATTTTGAATGGAATGGGAAAGTGCATTTTACTGTATTTTGTGTTTAT 2340
2702 TTTCCTGATTAATGGAAGAAATTTAAATGTCATATAAATTTTCTAGAGAGTAA 2758
2341 TTTCCTGATTAATGGAAGAAATTTAAATGTCATATAAATTTTCTAGAGAGTAA 2397

RESULT 3
AAPS4395
ID AAPS4395 standard; DNA; 2397 BP.
XX
AC AAPS4395;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #75.
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Feng S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PW, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
therapy.
XX
PS Claim 2; Fig 149; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.

CC	These proteins and the DNA encoding them may be used as hybridization									
CC	probes, in chromosome and gene mapping and in the generation of anti-									
CC	sense RNA and DNA. They may also be used to generate either									
CC	transgenic animals or knockout animals which are in turn useful for									
CC	development and screening of therapeutically useful reagents. The nucleic									
CC	acids may also be used in gene therapy									
XX										
SQ	Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;									
	Query Match	86.5%;	Score 2393.8;	DB 4;	Length 2397;					
	Best Local Similarity	99.9%;	Pred. No. 0;							
	Matches 2395;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;	
QY	362	AGAGAAAGACGCTCTCCAGCTGAAGCCAAATGACGCCCTCCGGCTCTCCCGCAGAGAGTT	421							
DB	1	AGAGAAAGACGCTCTCCAGCTGAAGCCAAATGACGCCCTCCGGCTCTCCCGCAGAGAGTT	60							
QY	422	CCCTGCCCGGATGAGCCCGCGCTGCGTCCCGACTATCCCGAGCGCGCTGGGCGAC	481							
DB	61	CCCTGCCCGGATGAGCCCGCGCTGCGTCCCGACTATCCCGAGCGCGCTGGGCGAC	120							
QY	482	CGGGCCAGCGCGACGATCGCTGCCGTTTGGCCCTTGGAGTAGGATGTGGTAAAGGA	541							
DB	121	CGGGCCAGCGCGACGATCGCTGCCGTTTGGCCCTTGGAGTAGGATGTGGTAAAGGA	180							
QY	542	TGGGGCTTCTCCCTTACGGGGCTCACAAATGCGCCAGAGAGATTCGGTGAAGTGTCTGCGC	601							
DB	181	TGGGGCTTCTCCCTTACGGGGCTCACAAATGCGCCAGAGAGATTCGGTGAAGTGTCTGCGC	240							
QY	602	TGCTGTCTTACGCCCTCAATCTGCTTTTGGTTAATGTCCTACGTGTGTGGCAGTT	661							
DB	241	TGCTGTCTTACGCCCTCAATCTGCTTTTGGTTAATGTCCTACGTGTGTGGCAGTT	300							
QY	662	TCCTCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTAACTCGAGAAACGAGGTA	721							
DB	301	TCCTCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTAACTCGAGAAACGAGGTA	360							
QY	722	GAGGAACAGTCAATTTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	781							
DB	361	GAGGAACAGTCAATTTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420							
QY	782	TGTTTCCCTTATCATTTGGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTTG	841							
DB	421	TGTTTCCCTTATCATTTGGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTTG	480							
QY	842	CTTCTTGCATGTTACTTTGGAAGTTTGCCTGTCTATTTCTGTGTAGAACCTGGCTTGGCG	901							
DB	481	CTTCTTGCATGTTACTTTGGAAGTTTGCCTGTCTATTTCTGTGTAGAACCTGGCTTGGCG	540							
QY	902	GTTTGGACATATGAACAGGAACCTTATGGTCCAGTCAATGGTCAGATATGGTCACCTTTG	961							
DB	541	GTTTGGACATATGAACAGGAACCTTATGGTCCAGTCAATGGTCAGATATGGTCACCTTTG	600							
QY	962	AAAGCCAGGATGACAAATATGAAATACCTAGATATCGGTGGCTTACTCATGCTTGAAT	1021							
DB	601	AAAGCCAGGATGACAAATATGAAATACCTAGATATCGGTGGCTTACTCATGCTTGAAT	660							
QY	1022	TTTTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACTGTTGGAATG	1081							
DB	661	TTTTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACTGTTGGAATG	720							
QY	1082	ACAGAGATGGAATGACCAATATGAAATACCTAGATATCGGTGGCTTACTCATGCTTGAAT	1141							
DB	721	ACAGAGATGGAATGACCAATATGAAATACCTAGATATCGGTGGCTTACTCATGCTTGAAT	780							
QY	1142	CAGGCCACCGAGGAGATCTCAGTGACCTTTATCAGAGGGTCTGGGAGAAATGTAT	1201							
DB	781	CAGGCCACCGAGGAGATCTCAGTGACCTTTATCAGAGGGTCTGGGAGAAATGTAT	840							
QY	1202	TCCCTTTTTCAGAGGAACCAACAACTGCGAGTGTCTGAGGTTCTCGGAAATCTCCATTGGG	1261							
DB	841	TCCCTTTTTCAGAGGAACCAACAACTGCGAGTGTCTGAGGTTCTCGGAAATCTCCATTGGG	900							

1262	GTGACAAATCTCGGCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT	1321
901	GTGACAAATCTCGGCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT	960
1322	AGAGGGAGCGCGGACAGACCAATGATGTCCTTTGAAGAAATGACAACTCTCAGCACCTG	1381
961	AGAGGGAGCGCTGGACAGACCAATGATGTCCTTTGAAGAAATGACAACTCTCAGCACCTG	1020
1382	TCATGTCCCTCAGTAGAACTGTTGAAACCCAGCCCTGTCAGAAATCTTTGAAACACATCC	1441
1021	TCATGTCCCTCAGTAGAACTGTTGAAACCCAGCCCTGTCAGAAATCTTTGAAACACATCC	1080
1442	ATGCGAACAGCTTTAATACACACTTTGAGATGAGGAGTTTATAAAAGAAATGTACAG	1501
1081	ATGCGAACAGCTTTAATACACACTTTGAGATGAGGAGTTTATAAAAGAAATGTACAG	1140
1502	AAGAAACCAACAACTTGTCTTACTGCACTTGTGAATTTTGTAGTACATCTATGTGTTT	1561
1141	AAGAAACCAACAACTTGTCTTACTGCACTTGTGAATTTTGTAGTACATCTATGTGTTT	1200
1562	CAGAAATATGTAGAAATATAAATGTTGCCATAAATTAACCTTAAGCATATCTATTCTA	1621
1201	CAGAAATATGTAGAAATATAAATGTTGCCATAAATTAACCTTAAGCATATCTATTCTA	1260
1622	TGCTTTAAATGAGGATGGAAGTTTCAATGTCATAAAGTCCACCCTGGGCAATATTTGA	1681
1261	TGCTTTAAATGAGGATGGAAGTTTCAATGTCATAAAGTCCACCCTGGGCAATATTTGA	1320
1682	TGCCCTTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGCTTTTA	1741
1321	TGCCCTTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGCTTTTA	1380
1742	CTGACACAGTTTGTGAGGAGCATGTTTGTAGTATGATTTAGCATTTCCGCAATCCATGCAA	1801
1381	CTGACACAGTTTGTGAGGAGCATGTTTGTAGTATGATTTAGCATTTCCGCAATCCATGCAA	1440
1802	CGAGTCACATATGCTGGGACCTGGAGCCATAGTAAAGTTGATTTTCTTACCACTAGT	1861
1441	CGAGTCACATATGCTGGGACCTGGAGCCATAGTAAAGTTGATTTTCTTACCACTAGT	1500
1862	ATATTAAGTACTAATTAATGCTTAACATAGGAGCTTAGAAATACTAATCTTTTATTA	1921
1501	ATATTAAGTACTAATTAATGCTTAACATAGGAGCTTAGAAATACTAATCTTTTATTA	1560
1922	CTCAGCGATCTATTCTTCTGATGCTAAATTAATATATATCAGAAAACTTTCAATATTGG	1981
1561	CTCAGCGATCTATTCTTCTGATGCTAAATTAATATATATCAGAAAACTTTCAATATTGG	1620
1982	TGACTACCAATGATGATTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATG	2041
1621	TGACTACCAATGATGATTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATG	1680
2042	GCTAACACATGCTTAACTGATCAGGAGTTTGTGATATAAGTCTGTGTTAAATCTG	2101
1681	GCTAACACATGCTTAACTGATCAGGAGTTTGTGATATAAGTCTGTGTTAAATCTG	1740
2102	TATTAATTCAGTCGATTTTCTGATTAATGATTAACCAATTAAGAAAGAAAT	2161
1741	TATTAATTCAGTCGATTTTCTGATTAATGATTAACCAATTAAGAAAGAAAT	1800
2162	TGTGCTCTGATAGCATCATTTTGTAGCCTTCTGTTAATAAGCTTTTACTATTCTGT	2221
1801	TGTGCTCTGATAGCATCATTTTGTAGCCTTCTGTTAATAAGCTTTTACTATTCTGT	1860
2222	CCTGGGCTTATATTAACATATACTGTTATTTAAATCTTTAAACCACTAATTTTGAAT	2281
1861	CCTGGGCTTATATTAACATATACTGTTATTTAAATCTTTAAACCACTAATTTTGAAT	1920
2282	TACCACTGTGATACATAGGAATCATTTTCCAGATGATGCTGCTTTTAGGAATTA	2341
1921	TACCACTGTGATACATAGGAATCATTTTCCAGATGATGCTGCTTTTAGGAATTA	1980
2342	ATAAGAAAAATTTGCACATAAATCTAGTTGATTCAGAAAAAGGACTTGTATGCTGCTTCTCC	2401

Db 1981 ATAAGAAAATTTGCACATACTTAGTTGATTCAGAAAAGGACTGTATGCTGTTTTCTCTCC 2040
Qy 2402 CAAATGAAGACTCTTTTGTACACTAAACACACTTTTTTAAAAAGCTTATCTTTGCGCTTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTGTACACTAAACACACTTTTTTAAAAAGCTTATCTTTGCGCTTCTCCA 2100
Qy 2462 AACGAAGCAATAGTCTCCAGTCAATATAAATCTTACAGAAAATAGTGTCTTTTCT 2521
Db 2101 AACGAAGCAATAGTCTCCAGTCAATATAAATCTTACAGAAAATAGTGTCTTTTCT 2160
Qy 2522 CCAGAAAATCTCTGTGAGAAATCAATTAACATGTCGCAATTTAGAGATCTTTTGTGTTTA 2581
Db 2161 CCAGAAAATCTCTGTGAGAAATCAATTAACATGTCGCAATTTAGAGATCTTTTGTGTTTA 2220
Qy 2582 TTTCACTGATTAATATCTGCGCAATTAACAGATTAATAATTTTTTCAAGAGTA 2641
Db 2221 TTTCACTGATTAATATCTGCGCAATTAACAGATTAATAATTTTTTCAAGAGTA 2280
Qy 2642 TAGTATATTTTGAATGGAAGTGCATTTTACTGTATTTTGTGTTATTTGTTAT 2701
Db 2281 TAGTATATTTTGAATGGAAGTGCATTTTACTGTATTTTGTGTTATTTGTTAT 2340
Qy 2702 TTTCTCAGATATGGAAGAAAATTAATAATGTGCAATAAATATTTTCTAGAGAGTAA 2758
Db 2341 TTTCTCAGATATGGAAGAAAATTAATAATGTGCAATAAATATTTTCTAGAGAGTAA 2397

RESULT 4
AAS46086
ID AAS46086 standard; cDNA; 2397 BP.
AC AAS46086;
XX
XX
DT 18-DEC-2001 (first entry)
DE
XX
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN W0200168848-A2.
XX
XX
PD 20-SEP-2001.
XX
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194493P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.

PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199554P.
PR 03-MAY-2000; 2000US-0201515P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX P-PSDB; AAU29185.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 323; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;
SQ

Query Match 86.5%; Score 2393.8; DB 4; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 362 AGAGAAAAGAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGTCTTCGCGAAGAAGTT 421
Db 1 AGAGAAAAGAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGTCTTCGCGAAGAAGTT 60
Qy 422 CCTGCCCCGATGAGCCCCCGCGTCCCGACTATCCCGAGCGCGGTGGGCAC 481
Db 61 CCTGCCCCGATGAGCCCCCGCGTCCCGACTATCCCGAGCGCGGTGGGCAC 120
Qy 482 CGGGCCCCAGCGCCGACGATCGCTGCGGTTTTTCCCTTGGAGTAGAGTGTGTGAAGAAG 541
Db 121 CGGGCCCCAGCGCCGACGATCGCTGCGGTTTTTCCCTTGGAGTAGAGTGTGTGAAGAAG 180
Qy 542 TGGGGCTTCTCCCTTACGGGGCTCAATGGCCAGAGAAGATTCGCTGAAGTGTCTGGCC 601
Db 181 TGGGGCTTCTCCCTTACGGGGCTCAATGGCCAGAGAAGATTCGCTGAAGTGTCTGGCC 240
Qy 602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTTAAATGTCCATCAGTGTGTGSCAGTT 661

Db 241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCATCCATGCTGTGTGGCAGTT 300
Qy 662 TCTGCTTGGATGAGGAGTACTTAATAATGTTCTCACTTAACTCGAGAAACAGGGTA 721
Db 301 TCTGCTTGGATGAGGAGTACTTAATAATGTTCTCACTTAACTCGAGAAACAGGGTA 360
Qy 722 GAGGAAGCAGTCAATTTGACCTTACTTTCCTGCTGCTTCACTCCGCTCAGATGCTGTTTC 781
Db 361 GAGGAAGCAGTCAATTTGACCTTACTTTCCTGCTGCTTCACTCCGCTCAGATGCTGTTTC 420
Qy 782 TGTTCCTTATCATGTTGGGGATGTTAGGATATGTTGGAACGCTGGAAGAAATCTGTTG 841
Db 421 TGTTCCTTATCATGTTGGGGATGTTAGGATATGTTGGAACGCTGGAAGAAATCTGTTG 480
Qy 842 CTTCTTGCACTGTTACTTTTGGAAAGTTGCTTGTCACTTTCCTGCTAGAACTGCTTGTGC 901
Db 481 CTTCTTGCACTGTTACTTTTGGAAAGTTGCTTGTCACTTTCCTGCTAGAACTGCTTGTGC 540
Qy 902 GTTTGGACATATGAACGAACTTATGTTTCCAGTACAAATGTTTCAGATATGTTCACTTTC 961
Db 541 GTTTGGACATATGAACGAACTTATGTTTCCAGTACAAATGTTTCAGATATGTTCACTTTC 600
Qy 962 AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGCTTGGAAAT 1021
Db 601 AAAGCCAGGATGACAAATATGGAATACCTAGATATCGGTGGCTTACTCATGCTTGGAAAT 660
Qy 1022 TTTTTCAGAGAGTTAATGCTGTGGAGTATGTTTCACTGACTGTTGGAATG 1081
Db 661 TTTTTCAGAGAGTTAATGCTGTGGAGTATGTTTCACTGACTGTTGGAATG 720
Qy 1082 ACAGAGATGACTGGCCCCAGATCTCTGCTGTTAGAGAAATCCAGGATGTTCCAAA 1141
Db 721 ACAGAGATGACTGGCCCCAGATCTCTGCTGTTAGAGAAATCCAGGATGTTCCAAA 780
Qy 1142 CAGCCCAACAGGAGATCTCAGTACCTTTATCAAGAGGGTTGTGGGAGAAATGTTAT 1201
Db 781 CAGCCCAACAGGAGATCTCAGTACCTTTATCAAGAGGGTTGTGGGAGAAATGTTAT 840
Qy 1202 TCCTTTTGGAGAGAACCAACACTCAGTGGCTGAGGTTCTGGGATCTCCATTTGG 1261
Db 841 TCCTTTTGGAGAGAACCAACACTCAGTGGCTGAGGTTCTGGGATCTCCATTTGG 900
Qy 1262 GTGACAAATCTCTGGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db 901 GTGACAAATCTCTGGCCATGATTTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy 1322 AGAAGGAGCGGGGACAGACCAATGATGTTCTTGAAGATGACAACTCTCAGCACCTG 1381
Db 961 AGAAGGAGCGGGGACAGACCAATGATGTTCTTGAAGATGACAACTCTCAGCACCTG 1020
Qy 1382 TCATGCTCCCTCAGTGAACCTGTTGAACCAAGCTGTCAAGATCTTTGAACACACATCC 1441
Db 1021 TCATGCTCCCTCAGTGAACCTGTTGAACCAAGCTGTCAAGATCTTTGAACACACATCC 1080
Qy 1442 ATGCCAAACAGCTTTAATAACACTTTGAGATGGAGGATTAATAAGAAATGTCACAG 1501
Db 1081 ATGCCAAACAGCTTTAATAACACTTTGAGATGGAGGATTAATAAGAAATGTCACAG 1140
Qy 1502 AAGAAACCAACAACTTTTACTGGACTTGTGAATTTTGGATGATCACTATGTTT 1561
Db 1141 AAGAAACCAACAACTTTTACTGGACTTGTGAATTTTGGATGATCACTATGTTT 1200
Qy 1562 CAGAAATATGTAGAAATTAATAATGTTGCCATAAATAACACCTTAAGCATATCTATCTA 1621
Db 1201 CAGAAATATGTAGAAATTAATAATGTTGCCATAAATAACACCTTAAGCATATCTATCTA 1260
Qy 1622 TGCCTTAAATGAGATGGAAGTTTCATGTCATAGTCCACCTGAGCATATCTGA 1681
Db 1261 TGCCTTAAATGAGATGGAAGTTTCATGTCATAGTCCACCTGAGCATATCTGA 1320
Qy 1682 TGCCTTAAATGAGATGGAAGTTTCATGTCATAGTCCACCTGTCATGCTGTATGACTTTTA 1741

Db 1321 TGCCTTAAATGAGATGGAAGTTTCATGTCATAGTCCACCTGTCATGCTGTATGACTTTTA 1380
Qy 1742 CTGAACACAGTTATGTTTGGAGGAGCATGGTTTGTATGATTTCCGCATTCATGCAAA 1801
Db 1381 CTGAACACAGTTATGTTTGGAGGAGCATGGTTTGTATGATTTCCGCATTCATGCAAA 1440
Qy 1802 CGAGTCACATATGTTGGGAGCTGGAGCCATAGTAAAGTTGATTTACTTTTACCAACTAGT 1861
Db 1441 CGAGTCACATATGTTGGGAGCTGGAGCCATAGTAAAGTTGATTTACTTTTACCAACTAGT 1500
Qy 1862 ATATAAGTACTAATAATTAATGCTTAACATAGGAAGTTAGAAAATACTAATACTTTTATTA 1921
Db 1501 ATATAAGTACTAATAATTAATGCTTAACATAGGAAGTTAGAAAATACTAATACTTTTATTA 1560
Qy 1922 CTCAGCGATCTATTTCTGATGCTAATAATTAATTAATATATACGAAACTTTCAATATGG 1981
Db 1561 CTCAGCGATCTATTTCTGATGCTAATAATTAATTAATATATACGAAACTTTCAATATGG 1620
Qy 1982 TGACTACCTAATGCTGATTTTCTGCTGTTACTAATAATTTCTTACCACCTTAAAGAGCAA 2041
Db 1621 TGACTACCTAATGCTGATTTTCTGCTGTTACTAATAATTTCTTACCACCTTAAAGAGCAA 1680
Qy 2042 GCTAACACATTTGCTTAAGCTGATCAGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db 1681 GCTAACACATTTGCTTAAGCTGATCAGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740
Qy 2102 TATAATTCAGTCGATTTTCTGATGCTAATAATGTTAAGAAATACCAATTAATAAGAGAAAT 2161
Db 1741 TATAATTCAGTCGATTTTCTGATGCTAATAATGTTAAGAAATACCAATTAATAAGAGAAAT 1800
Qy 2162 TTGCTCTGTATAGCATCATTTTATAGCCCTTCTCTGTTAATAAGCTTTACTATCTGT 2221
Db 1801 TTGCTCTGTATAGCATCATTTTATAGCCCTTCTCTGTTAATAAGCTTTACTATCTGT 1860
Qy 2222 CTGGGCTTATATTACACATATACTGTTTAAATTAATTAATTAATTAATTAATTAATTAAT 2281
Db 1861 CTGGGCTTATATTACACATATACTGTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1920
Qy 2282 TACAGTGTGATACATAGGAATCATTTTACAGAAATGATGCTGCTTTTAGGAAGTATTA 2341
Db 1921 TACAGTGTGATACATAGGAATCATTTTACAGAAATGATGCTGCTTTTAGGAAGTATTA 1980
Qy 2342 ATAGAAATTTGACATATACTAGTTGATTCAGAAAGGACTGTATGCTGTTTCTTCC 2401
Db 1981 ATAGAAATTTGACATATACTAGTTGATTCAGAAAGGACTGTATGCTGTTTCTTCC 2040
Qy 2402 CAAATGAAGACTCTTTTGTGACCTAAACACTTTTAAATAAGCTTTATCTTGGCTTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTGTGACCTAAACACTTTTAAATAAGCTTTATCTTGGCTTCTCCA 2100
Qy 2462 AACAGAGCAATAGTCTCCAACTCAATAATAATTTTACAGAAATAGTGTCTTTTCT 2521
Db 2101 AACAGAGCAATAGTCTCCAACTCAATAATAATTTTACAGAAATAGTGTCTTTTCT 2160
Qy 2522 CCAGAAATCTGTTGAGAAATCAATAAATCAATGATGCAATTTAGAGATCTTTGTTT 2581
Db 2161 CCAGAAATCTGTTGAGAAATCAATAAATCAATGATGCAATTTAGAGATCTTTGTTT 2220
Qy 2582 TTTCACTGATTAATATAGTCTGGCAAAATTAACAGATTTTAAATTTTAAAGAGTA 2641
Db 2221 TTTCACTGATTAATATAGTCTGGCAAAATTAACAGATTTTAAATTTTAAAGAGTA 2280
Qy 2642 TAGTATATTTTGAATGGAAAGTGCATTTTACTGTTTGTATTTTGTGTTAT 2701
Db 2281 TAGTATATTTTGAATGGAAAGTGCATTTTACTGTTTGTATTTTGTGTTAT 2340
Qy 2702 TTTCTCAGAAATGGAAGAAATTTAAATGTTCAATAAATTTTCTAGAGAGTAA 2758
Db 2341 TTTCTCAGAAATGGAAGAAATTTAAATGTTCAATAAATTTTCTAGAGAGTAA 2397

ID XX AAF92111 standard; cDNA; 2397 BP.
AC AAF92111;
XX 15-MAY-2001 (first entry)
DT XX Human PRO1568 cDNA.
XX Human, PRO protein; mapping; ss.
XX Homo sapiens.
OS W0200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-US023328.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 07-DEC-1999; 99US-0169495P.
XX 09-DEC-1999; 99US-0170282P.
XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 03-MAR-2000; 2000US-0187202P.
XX 21-MAR-2000; 2000US-0191007P.
XX 30-MAR-2000; 2000WO-US008439.
XX 25-APR-2000; 2000US-0199397P.
XX 22-MAY-2000; 2000WO-US014042.
XX 05-JUN-2000; 2000US-0209832P.
PA (GETH) GENENTECH INC.
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2001-183260/18.
XX P-PSDB; AAB87579.
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX Claim 2; Fig 107; 278bp; English.
XX The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX SQ Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;
Query Match 85.5%; Score 2393.8; DB 4; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 362 AGAAGAAGAGCGTCTCCAGCTGAAGCCCAATGACGCCCTCCGGCTCTCCCGAAGATT 421
Db 1 AGAAGAAGAGCGTCTCCAGCTGAAGCCCAATGACGCCCTCCGGCTCTCCCGAAGATT 60
Qy 422 CCCTGCCCGATGAGCCCGCGGTCTCCCGACTATCCAGCGCGCGGTGGGCAC 481
Db 61 CCCTGCCCGATGAGCCCGCGGTCTCCCGACTATCCAGCGCGCGGTGGGCAC 120
Qy 482 CGGCGCCGAGCCGACGATCGTCCCGTTTGGCGGTAGGATGTGTGAAGGA 541

Db 121 CGGGCCAGCGCGAGGATCGCTCGCTTTGGCCCTGGAGTAGGATGTGTGAAGGA 180
Qy 542 TGGGGCTTCTCCCTTACGGGGCTCAATATGGCCAGAGAGATTCGTGAAGTGTCTGGCC 601
Db 181 TGGGGCTTCTCCCTTACGGGGCTCAATATGGCCAGAGAGATTCGTGAAGTGTCTGGCC 240
Qy 602 TGCCTGCTCTACGCCCTCAATCTCTCTTTTGGTTAAATGTCCATCAGTGTGTGGCAGTT 661
Db 241 TGCCTGCTCTACGCCCTCAATCTCTCTTTTGGTTAAATGTCCATCAGTGTGTGGCAGTT 300
Qy 662 TCTGTTGGATGAGGGACTACCTAAATAANGTCTCACTTTAACTGCAAGAAAGAGGTA 721
Db 301 TCTGTTGGATGAGGGACTACCTAAATAANGTCTCACTTTAACTGCAAGAAAGAGGTA 360
Qy 722 GAGGAGCAGTCAATTTGACTTCTCTGTTGTTTCTCGGTTCATCGGTTCATGTTGCTTTGC 781
Db 361 GAGGAGCAGTCAATTTGACTTCTCTGTTGTTTCTCGGTTCATCGGTTCATGTTGCTTTGC 420
Qy 782 TGTTCCTTATCATTTGTTGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTTG 841
Db 421 TGTTCCTTATCATTTGTTGGGATGTTAGGATATTTGGAAACGGTGAAGAAATCTGTTG 480
Qy 842 CTCTTGCATGTACTTTGGAAGTTTCTGTCTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db 481 CTCTTGCATGTACTTTGGAAGTTTCTGTCTCATTTTCTGTGTAGAACTGGCTTGTGGC 540
Qy 902 GTTTGGACATATGAACAGAACTTATGTTTCCAGTACAATGGTCAAGATGGTCACTTTG 961
Db 541 GTTTGGACATATGAACAGAACTTATGTTTCCAGTACAATGGTCAAGATGGTCACTTTG 600
Qy 962 AAAGCCAGGATGACAAATATGATTAAGTATCTAGATATCGGTGGCTTACTGCTTGGAT 1021
Db 601 AAAGCCAGGATGACAAATATGATTAAGTATCTAGATATCGGTGGCTTACTGCTTGGAT 660
Qy 1022 TTTTTCAGAGAGTTTAAAGTCTGGAGTAGTATATTTCACTGACTGTTGGAATG 1081
Db 661 TTTTTCAGAGAGTTTAAAGTCTGGAGTAGTATATTTCACTGACTGTTGGAATG 720
Qy 1082 ACAGAGATGACTGGCCCCCAGATTCTCTGTGTGTAGAGAAATCCCAAGGATGTTCCAAA 1141
Db 721 ACAGAGATGACTGGCCCCCAGATTCTCTGTGTGTAGAGAAATCCCAAGGATGTTCCAAA 780
Qy 1142 CAGGGCCACAGAGATCTCAGTCACTTATCAAGAGGTTTGGGAAGAAATGAT 1201
Db 781 CAGGGCCACAGAGATCTCAGTCACTTATCAAGAGGTTTGGGAAGAAATGAT 840
Qy 1202 TCTTTTGGAGAGAACCAACAACTGCAGGTGCTGAGGTTCTCGGAATCTCCATGGG 1261
Db 841 TCTTTTGGAGAGAACCAACAACTGCAGGTGCTGAGGTTCTCGGAATCTCCATGGG 900
Qy 1262 GTGACACAAATCCTGGCCATGATTCTACCAATCTCTGCTCTGGGCTCTGTATTATGAT 1321
Db 901 GTGACACAAATCCTGGCCATGATTCTACCAATCTCTGCTCTGGGCTCTGTATTATGAT 960
Qy 1322 AGAAGGAGCGGGGACAGCCCAATGATGCTTGAAGATGACAACTCTCAGCACCTG 1381
Db 961 AGAAGGAGCGCGGACAGCCCAATGATGCTTGAAGATGACAACTCTCAGCACCTG 1020
Qy 1382 TCATGTCCCTCAGTAGAATGTTTGAACCAAGSCCTGTCAAGAAATCTTTGAACACATCC 1441
Db 1021 TCATGTCCCTCAGTAGAATGTTTGAACCAAGSCCTGTCAAGAAATCTTTGAACACATCC 1080
Qy 1442 ATGGGCAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAGAAATGTACAG 1501
Db 1081 ATGGGCAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAGAAATGTACAG 1140
Qy 1502 AAGAAACACAAACTTTGTTTACTGGACTTGTGAATTTTGGTACATCTATGTGTT 1561
Db 1141 AAGAAACACAAACTTTGTTTACTGGACTTGTGAATTTTGGTACATCTATGTGTT 1200
Qy 1562 CAGAAATATGTGAATAAATAAATGTTGCCATTAATAACACCTAAGCATATCTATTCTA 1621

Db 1201 CAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACACCTAAGCATATATCTTCTA 1260
Qy 1622 TGCTTTAAATGAGTGAAGTTCATGTCATTAAGTCACACCTGGACATATTCGA 1681
Db 1261 TGCTTTAAATGAGTGAAGTTCATGTCATTAAGTCACACCTGGACATATTCGA 1320
Qy 1682 TGCCCTTAAATGCTGAAGACAGATGTCATPACCACCTGTGTGTCCTGTGTATGACTTTTA 1741
Db 1321 TGCCCTTAAATGCTGAAGACAGATGTCATPACCACCTGTGTGTCCTGTGTATGACTTTTA 1380
Qy 1742 CTGAACACAGTTATGTTTTCAGGACAGATGTTTGAATAGCATTTCCGCATCCATGCAAA 1801
Db 1381 CTGAACACAGTTATGTTTTCAGGACAGATGTTTGAATAGCATTTCCGCATCCATGCAAA 1440
Qy 1802 CGAGTCACATATGTTGGGACCTGGAGCCATAGTAAAGCTTGATTACTTCTTACCACCTAGT 1861
Db 1441 CGAGTCACATATGTTGGGACCTGGAGCCATAGTAAAGCTTGATTACTTCTTACCACCTAGT 1500
Qy 1862 ATATAAGTACTAATTAATGCTTAACATAGGAAGTTAGAAATACATAAATCTTTTATTA 1921
Db 1501 ATATAAGTACTAATTAATGCTTAACATAGGAAGTTAGAAATACATAAATCTTTTATTA 1560
Qy 1922 CTGAGCATCTATCTTCTGATGCTTAATAAATATATATATCAGAAACCTTTCATATTCGG 1981
Db 1561 CTGAGCATCTATCTTCTGATGCTTAATAAATATATATATCAGAAACCTTTCATATTCGG 1620
Qy 1982 TGACTACCTAAATGTTGATTTTCTGCTGTTACTAAATATTTCTTACCACCTTAAAGACAA 2041
Db 1621 TGACTACCTAAATGTTGATTTTCTGCTGTTACTAAATATTTCTTACCACCTTAAAGACAA 1680
Qy 2042 GCTAACACATGCTTAAGCTGATCAGGATTTTGTATATATAGTCTGTGTATATCTG 2101
Db 1681 GCTAACACATGCTTAAGCTGATCAGGATTTTGTATATATAGTCTGTGTATATCTG 1740
Qy 2102 TATAAATTCAGTCGATTTTCAGTCTGATTAATGTTTAAAGAAATACCATTTATGAAAGGAAAT 2161
Db 1741 TATAAATTCAGTCGATTTTCAGTCTGATTAATGTTTAAAGAAATACCATTTATGAAAGGAAAT 1800
Qy 2162 TTGTCCTGTTAGATCATTTATTTTAGCCTTTCCTGTTTAAAGAAATACCATTTATGAAAGGAAAT 2221
Db 1801 TTGTCCTGTTAGATCATTTATTTTAGCCTTTCCTGTTTAAAGAAATACCATTTATGAAAGGAAAT 1860
Qy 2222 CCTGGGCTTATTTACACATATTAATGTTTAAATACCTTAAACCACTAATTTTGAAT 2281
Db 1861 CCTGGGCTTATTTACACATATTAATGTTTAAATACCTTAAACCACTAATTTTGAAT 1920
Qy 2282 TACCAGTGTATACATAGGAATCATTTATTCAGAAATGAGTCTGGTCTTTAGGAAGTATTA 2341
Db 1921 TACCAGTGTATACATAGGAATCATTTATTCAGAAATGAGTCTGGTCTTTAGGAAGTATTA 1980
Qy 2342 ATAGAATTTTACACATATTTAGTGTATTCAGAAAGGACCTGTATGTTCTCTCC 2401
Db 1981 ATAGAATTTTACACATATTTAGTGTATTCAGAAAGGACCTGTATGTTCTCTCC 2040
Qy 2402 CAAATGAAGACTCTTTTTCGACCTAAACACTTTTAAAGGCTTATCTTTGCTCTCCA 2461
Db 2041 CAAATGAAGACTCTTTTTCGACCTAAACACTTTTAAAGGCTTATCTTTGCTCTCCA 2100
Qy 2462 AACAGGAAGCAATGCTTCCAGTCAATATAAATCTACAGAAATAGTGTCTTTTCT 2521
Db 2101 AACAGGAAGCAATGCTTCCAGTCAATATAAATCTACAGAAATAGTGTCTTTTCT 2160
Qy 2522 CCAGAAATGCTTGTGAGAAATCATTAACACATGTCACAAATTTAGAGATCTTTGTTT 2581
Db 2161 CCAGAAATGCTTGTGAGAAATCATTAACACATGTCACAAATTTAGAGATCTTTGTTT 2220
Qy 2582 TTTCACGTATATATATCTGTCGCAATATACAGATTAATAATTTTACAGAGTA 2641
Db 2221 TTTCACGTATATATATCTGTCGCAATATACAGATTAATAATTTTACAGAGTA 2280
Qy 2642 TAGTATATTTATTTGAATGGGAAAGTGCATTTTCTGTTATTTGTTTAT 2701
Db 2281 TAGTATATTTATTTGAATGGGAAAGTGCATTTTCTGTTATTTGTTTAT 2340

Qy 2702 TTCTCAGATATGGAAGAAATTTAAATTTGTTCAATAAATATTTCTAGAGATTA 2758
Db 2341 TTCTCAGATATGGAAGAAATTTAAATTTGTTCAATAAATATTTCTAGAGATTA 2397
RESULT 6
ABS74431
ID ABS74431 standard; cDNA; 2397 BP.
XX
AC ABS74431;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1568.
XX
KW Human; ss: gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0098763P.
PR 10-SEP-1998; 98US-0098792P.
PR 10-SEP-1998; 98US-0098812P.
PR 16-SEP-1998; 98US-0098815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.

PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 10-NOV-2000; 2000WO-US030873.
PR 20-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2002-731348/79.
DR P-PSDB; ABG95904.

XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 107; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, C/G, D/H or E/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for

CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention

XX
SQ Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

Query Match 86.5%; Score 2393.8; DB 6; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 482 CGGGCCCCAGCGCCGACAGTCGCTGCCGTTTGGCCCTTGGGAGTAGAGTGTGTGAAAGGA 541
DB 121 CGGGCCCCAGCGCCGACAGTCGCTGCCGTTTGGCCCTTGGGAGTAGAGTGTGTGAAAGGA 180
QY 542 TGGGGCTCTCCCTTACGGGGCTCAATGCCAGAGAGATTCGCTGAAGTGTCTGGCG 601
DB 181 TGGGGCTCTCCCTTACGGGGCTCAATGCCAGAGAGATTCGCTGAAGTGTCTGGCG 240
QY 602 TGCCTGTCTACGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTGGCAGTT 661
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DB 301 TGTGCTGGATGAGGAGTACCTAATAATGTCTCATTCTTAACTTGAACGAGAGGTA 360
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RESULT 7

ABX78689
ID ABX78689 standard; cDNA; 2397 BP.

XX AC ABX78689;

XX DT 15-APR-2003 (first entry)

XX XX Human PRO polynucleotide #162.

XX DE Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX FN US2003027272-A1.

XX PD 06-FEB-2003.

XX PF 21-JUN-2002; 2002US-00176492.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0063120P.

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DB 2341 TTCTCAGATATGGAAGAAATTTAAATGTCATTAATAATTTTCTAGAGAGTAA 2397

RESULT 8
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ID ACA75661 standard; cDNA; 2397 BP.
AC ACA75661;
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DT 07-JUL-2003 (first entry)
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DE Novel human secreted and transmembrane protein PRO1568 cDNA.
XX
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
XX
OS Homo sapiens.
XX
XX
FN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
XX
PF 26-JUN-2002; 2002US-00183012.
XX
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PR 06-OCT-1998; 98US-0103258P.

Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 AGAGAAAGAGCGTCTCAGCTGAAGCCAAATGACGACCTCCGGCTCTCCCGAAGAGTT 60
QY 422 CCCTGCCCGGATGAGCCCGCGCGTGGTCCCGACTATCCGAGCGGGCGTGGGGCAC 481
DB 61 CCCTGCCCGGATGAGCCCGCGCGTGGTCCCGACTATCCGAGCGGGCGTGGGGCAC 120
QY 482 CGGGCCCGAGCGCCGACGATCGCTGCCCTTTGGCTTTGGGAGTAGGATGGTGAAGGA 541
DB 121 CGGGCCCGAGCGCCGACGATCGCTGCCCTTTGGCTTTGGGAGTAGGATGGTGAAGGA 180
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QY 602 TGCTGCTCTACGCCCTCAATCTGCTTTTGGTTAATGTCATCATGTTGGCAGTT 661
DB 241 TGCTGCTCTACGCCCTCAATCTGCTTTTGGTTAATGTCATCATGTTGGCAGTT 300
QY 662 TCTGCTTGGATGAGGAGTACTACCTAAATATGTTCTCACTTTAACTCGAGAAACGAGGTA 721
DB 301 TCTGCTTGGATGAGGAGTACTACCTAAATATGTTCTCACTTTAACTCGAGAAACGAGGTA 360
QY 722 GAGGAGCAGTCACTTTGACTTACTTCCGTCGTCATCCGCTCATGTTGGTGTTC 781
DB 361 GAGGAGCAGTCACTTTGACTTACTTCCGTCGTCATCCGCTCATGTTGGTGTTC 420
QY 782 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGAAACCGTGAAGAAATCTGTTG 841
DB 421 TGTTTCTTATCATTTGTTGGGATGTTAGGATATTTGGAAACCGTGAAGAAATCTGTTG 480
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Qy 1142 |CAGGCCACAGAGAGATCTCAGTGACCTTTATCAAGAGGTTGTGGAGAAATGTAT 1201
Db 781 |CAGGCCACAGAGAGATCTCAGTGACCTTTATCAAGAGGTTGTGGAGAAATGTAT 840
Qy 1202 |TCCCTTTTGGAGAGAACCAACAACTGCAGGTTCTCGAGGTTTCTGGGAATCTCCATGGG 1261
Db 841 |TCCCTTTTGGAGAGAACCAACAACTGCAGGTTCTCGAGGTTTCTGGGAATCTCCATGGG 900
Qy 1262 |GTGACACAAATCTGGCCATGATTTCTACCATTTCTGCTCTGGGCTCTGTATATGAT 1321
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Qy 1322 |AGAGGGGCGGGGACAGACCAATGATGTCCTTGAAGAAAGACAACTCTCAGCACCTG 1381
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Qy 1382 |TCATGTCCTTCAGTAGAAGCTGTTGAAACCAAGCCTGTCAAGAACTTTTGAACACATCC 1441
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Qy 1742 |CTGAACACAGTTATGTTTGGAGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAA 1801
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Qy 1802 |CGAGTCACATATGTTGGACCTGGAGCCATAGTAAAGTTGATTACTTCTACCAACTAGT 1861
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Qy 1862 |ATATAAGTACTAATATAAGTCTAACATAGAGAGTTAGAAATATACTAATCTTTATTA 1921
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Qy 2222 |CTCGGCTTATATTACACATATAAAGCTGTTTAAATACTTAACCACTAATTTTGAAGAT 2281
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RESULT 9

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ID ACA71141 standard; cDNA; 2397 BP.

XX ACA71141;

XX 02-AUG-2003 (first entry)

XX Human secreted/transmembrane protein (PRO) cDNA #162.

XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.

XX Homo sapiens.

XX US2003032112-A1.

XX 13-FEB-2003.

XX 21-JUN-2002; 2002US-00176756.

XX 18-SEP-1997; 97US-0059263P.

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Best Local Similarity 99.98; Pred. No. 0;
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QY 2282 TACCAAGTGTATACATAGGAATCAATTAATTCAGAAATGAGTCTGCTTTAGGAAGTATTA 2341
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RESULT 10
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ID ACC87669 standard; cdna; 2397 BP.
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AC ACC87669;
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DT 05-AUG-2003 (first entry)
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DE Human secreted polypeptide PRO1568-encoding cdna, SEQ ID NO:323.
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KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
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PN US2003027278-A1.
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PD 06-FEB-2003.
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FF 21-JUN-2002; 2002US-00176987.
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FF 18-SEP-1997; 97US-0059263P.
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RESULT 11

ACC87055
ID ACC87055 standard; cdna; 2397 BP.

XX AC ACC87055;

DT DT 05-AUG-2003 (first entry)

XX Human secreted polypeptide PRO1568-encoding cdna, SEQ ID NO:323.

DE Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.

XX Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

XX

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XX	18-SEP-1997;	97US-0059263P.	
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PR	16-SEP-1998;	98US-0101751P.	QY	1022	TTTTTTTCAGAGAGATTTAAGTCTGTGAGTAGTATATTTCACTGACTGCTTGGAAATG	1081
PR	16-SEP-1998;	98WO-US019330.	DB	661	TTTTTTTCAGAGAGATTTAAGTCTGTGAGTAGTATATTTCACTGACTGCTTGGAAATG	720
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PR	17-SEP-1998;	98US-0100930P.	QY	1142	CAGGCCACAGGAAGATCTCAGTGAACCTTTATCAAGAGGGTGTGGAGAGAAATGTAT	1201
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PR	23-SEP-1998;	98US-0101471P.	QY	1202	TCCTTTTTGAGAGAAACCAACAACTGAGGCTGTGAGGTTCTCGGAAATCTCCATTGGG	1261
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PR	29-SEP-1998;	98US-0102330P.	DB	1081	ATGCAAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAGAAATGTACAG	1140
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PR	01-OCT-1998;	98US-0102687P.	QY	1622	TGCTTTAAATGAGGATGGAAAGTTTCATGTCATAGTCACCCACTGTGTAGCCTGTGATGACITTTA	1681
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PR	01-OCT-1998;	98US-0102687P.	DB	1501	ATATAAGTACTAATTAATGCTTAACATAGAGAGTTAGAAATACTAATACTTTTATTA	1560
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Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1981 ATAAGAAAATTTGCACATACTTAGTTGATTCAGAAAAGGACTTGTATGCTGTTTCTCC 2040
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Qy 2702 TTCTCAGATATGGAAGAAAATTAATATGTCATTAATATTTTCTAGAGTAA 2758
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RESULT 12

ACD04228 standard; cDNA; 2397 BP.

ID ACD04228

XX AC ACD04228;

XX AC ACD04228; (first entry)

XX DT 09-AUG-2003

XX DE Human secreted/transmembrane protein (PRO) cDNA #162.

XX XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;

XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

XX KW tissue typing.

XX OS Homo sapiens.

XX XX US2003040070-A1.

XX XX 27-FEB-2003.

XX XX 27-JUN-2002; 2002US-00184627.

XX 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0062250P.
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PR	25-JUN-1998;	98US-0090694P.	PR	06-OCT-1998;	98US-0103258P.
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QY	422	CCCTGCCCCGATGAGCCCCCGCTGCTCCCGACTATCCCGAGCGCGGCGTGGGCAC	481	CCCTGCCCCGATGAGCCCCCGCTGCTCCCGACTATCCCGAGCGCGGCGTGGGCAC	541
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QY	482	CGGCCCCAGCGCCGACGATCGCTGCGCTTTGCCCTTGGGAGTAGGATGTTGTAAGGA	541	CGGCCCCAGCGCCGACGATCGCTGCGCTTTGCCCTTGGGAGTAGGATGTTGTAAGGA	601
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QY	542	TGGGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGATTCCGTGAAGTGTCTGCGC	601	TGGGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGATTCCGTGAAGTGTCTGCGC	661
DB	181	TGGGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGATTCCGTGAAGTGTCTGCGC	240	TGGGCTTCTCCCTTACCGGGCTCACAATGCGGAGAGATTCCGTGAAGTGTCTGCGC	721
QY	602	TGCTGTCTACGCGCTCAATCTCTTTTGGTTAATGTCATCATGTTGGCAGTT	661	TGCTGTCTACGCGCTCAATCTCTTTTGGTTAATGTCATCATGTTGGCAGTT	781
DB	241	TGCTGTCTACGCGCTCAATCTCTTTTGGTTAATGTCATCATGTTGGCAGTT	300	TGCTGTCTACGCGCTCAATCTCTTTTGGTTAATGTCATCATGTTGGCAGTT	841
QY	662	TCTGCTTGATGAGGACTACTTAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	721	TCTGCTTGATGAGGACTACTTAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	841
DB	301	TCTGCTTGATGAGGACTACTTAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	360	TCTGCTTGATGAGGACTACTTAATAATGTTCTCACTTTAACTGAGAAACGAGGTA	420
QY	722	GAGGAAGCAGTCATTTGACTTACTTCTGTGTTTCACTCGGTCATGATGTTGTC	781	GAGGAAGCAGTCATTTGACTTACTTCTGTGTTTCACTCGGTCATGATGTTGTC	841
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DB	421	TGTTTCTTATCATGTTGGGATGTTAGGATTTGTTGAAAGGTTGAAAGGTTGTTG	901	TGTTTCTTATCATGTTGGGATGTTAGGATTTGTTGAAAGGTTGAAAGGTTGTTG	961
QY	842	CTTCTTGATGAGTACTTTTGAAGTTTCTGCTCACTTTTCTGTTAGAACTGCTTGTG	901	CTTCTTGATGAGTACTTTTGAAGTTTCTGCTCACTTTTCTGTTAGAACTGCTTGTG	961


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PR 10-SEP-1998; 98US-0099812P.
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Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 61 CCCTGCCCGATGAGCCCGCCGCTGGTCCCGACTATCCCGAGCGCGCGTGGGCAC 120.
QY 482 CGGGCCAGCGCGAGATCGTCCGCTTTTCCCTTTGGGAGTAGGATGTGGTGAAGGA 541
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QY 542 TGGGCGTCTCCCTTACCGGCTCACAATGGCCGAGAGAGTTCGGTGAAGTGTCTGCGC 601
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DB 301 TCTGCTTGGATGAGGAGTACTAAATAATGTCTCACTTTAACTGCAGAAACAGGGGTA 360
QY 722 GAGGAGAGAGTCAATTTGACTTACTTCTGCTGGTTCATCCGCTCATGATGCTTTTTCG 781
DB 361 GAGGAGAGAGTCAATTTGACTTACTTCTGCTGGTTCATCCGCTCATGATGCTTTTTCG 420
QY 782 TGTTCCTTATCATTTGCGGATGTAGGATATCTGGAACTGGTGAAGAAATCTGTG 841
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DB 481 CTTCTTCATCGTACTTTTGAAGTTTCTCTCTCAATTTCTGTAGAACTCGCTTGTGGC 540
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PR	10-JUN-1998;	98US-0088738P.	PR	16-SEP-1998;	98US-0100662P.	Db	181	TGGGGCTTCTCCCTTACGGGGCTCAATGCCCGAGAGATTCCTGAGTGTCTGCGC	240
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KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
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Job time : 1064.17 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 07:47:11 ; Search time 7165.47 Seconds

(without alignments)
11535.678 Million cell updates/sec

Title: US-09-830-328C-4

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em_estmu:*

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10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estom:*

16: em_eston:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

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27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	815.4	29.5	1201	13 BX384369	BX384369 BX384369

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ALIGNMENTS

RESULT 1

AK050737

LOCUS

DEFINITION

AK050737 2491 bp mRNA linear HTC 20-BEP-2003

Mus musculus 9 days embryo whole body cDNA, RIKEN full-length

enriched library clone.D030012P12 product:TETRAPAN NET-2 homolog

(Homo sapiens), full insert sequence.

ACCESSION

AK050737

VERSION

AK050737.1 GI:26341473

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Muridae; Mus.

REFERENCE

1

Carrincci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

Carrincci, P., Shihata, Y., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

20499374

MEDLINE

11042159

PUBMED

11042159

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	D	b	1011	TTCCTGGAAATCCATTTGGGTGACACAAATCCTGCCATGATCTCACCATCTACTCTGC	1070
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	Q	y	1952	AATTTATATATCAGAAAACTTTCAATATGTTGTGACTACTAAATGTGATTTTGTGTGTTA	2011
	D	b	1700	GATTTATATG-CAAAAATCTTTCAAGATTGGTGACTACTTAATAATGATTTTGTGTGTTA	1758
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 2463 AAAATTAA-----TCAATAAATTTTCTTACA 2489

 RESULT 2
 AK033554
 LOCUS
 DEFINITION Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030619B17 product:TETRAPAN NET-2 homolog [Homo sapiens], full insert sequence.
 ACCESSION AK033554
 VERSION AK033554.1 GI:26329230
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 AUTHORS Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, I., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Ishikawa, T., Inoue, Y., Kita, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE	20530913	ORIGIN	Query Match	42.6%; Score 1178; DB 11; Length 2325;
PUBMED	11076861		Best Local Similarity	74.7%; Pred. No. 8.9e-211;
REFERENCE	4		Matches 1785; Conservative	0; Mismatches 215; Indels 88; Gaps 21;
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL	Nature 420, 563-573 (2002)			
REFERENCE	6 (bases 1 to 2325)			
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, F., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/			
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RESULT 3
AY416016 918 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM5750 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY416016
VERSION AY416016.1 GI:39771976
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 918)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 918)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Db      959 AA 960

RESULT 5
BG210632/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 846)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
2127151
11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com
High quality sequence stop: 512.
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/cell_line="H1080"
/clone_lib="Athersys RAGE library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is H1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in H1080 under normal circumstances."

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Db      784 ATTTCATTCTTCCCACTAGTATATAAAGTACTATTAATTAATCTAACAATAGAACTTAGAA 725
Qy      1902 AATACATAAATCTTTTATTACTCAGCGCATCTATTCTTCTGATGCTAAATAAATATATAT 1961
Db      724 AATACATAAATCTTTTATTACTCAGCGCATCTATTCTTCTGATGCTAAATAAATATATAT 665
Qy      1962 CAGAAACTTTCATATTTGGTGAATCTTAACTTAATCTGATTTTGGTGGTACTTAAATATT 2021
Db      664 CAGAAACTTTCATATTTGGTGAATCTTAACTTAATCTGATTTTGGTGGTACTTAAATATT 605
Qy      2022 CTTTACCCTTAAAGAGCAAGCAATCAATTTCTTAAGCTGATCAGGGAATTTTTCGTAT 2081
Db      604 CTTTACCCTTAAAGAGCAAGCAATTTCTTAAGCTGATCAGGGAATTTTTCGTAT 545
Qy      2082 ATAAGTCTGTGTTAAATCTGTATTAATTCAGTCGATTTTCAAGTCTGATAAATGTTAAGAATA 2141
Db      544 ATAAGTCTGTGTTAAATCTGTATTAATTCAGTCGATTTTCAAGTCTGATAAATGTTAAGAATA 485
Qy      2142 ACCATTATGAAAGGAAATTTGCTCTGATAGCATCATTTATTTTAGCCCTTTCCTCTTA 2201
Db      484 ACCATTATGAAAGGAAATTTGCTCTGATAGCATCATTTATTTTAGCCCTTTCCTCTTA 425
Qy      2202 ATAAAGCTTTACTATTTCTGCTGGCTTATATTAACATATTAACATCTGTTATTTAAATACT 2261
Db      424 ATAAAGCTTTACTATTTCTGCTGGCTTATATTAACATATTAACATCTGTTATTTAAATACT 365
Qy      2262 TAAACACTAAATTTGAAATTTACCAGTCTGATACATAGGAATCATTTATTCAGAAATGAGT 2321
Db      364 TAAACACTAAATTTGAAATTTACCAGTCTGATACATAGGAATCATTTATTCAGAAATGAGT 305
Qy      2322 CTGGTCTTTAGAGATTAATAAGAAATTTGGACATAACTTAGTTGATTCAGAAAGGA 2381
Db      304 CTGGTCTTTAGAGATTAATAAGAAATTTGGACATAACTTAGTTGATTCAGAAAGGA 245
Qy      2382 CTGTATGCTGTTTCTTCCCAATGAAGACTCTTTTGGACACTAAACACTTTTAAAAA 2441
Db      244 CTGTATGCTGTTTCTTCCCAATGAAGACTCTTTTGGACACTAAACACTTTTAAAAA 195
Qy      2442 GCTATATCTTCTCTCCAAACAAAGCAAGCAATAGTCTCCAAAGTCAATATAAATTCACA 2501
Db      184 GCTATATCTTCTCTCCAAACAAAGCAAGCAATAGTCTCCAAAGTCAATATAAATTCACA 125
Qy      2502 GAAATAGTGTCTTTTCTCCAGAAAAATGCTTGTGAGAAATCATTTAAACATGTGACAA 2561
Db      124 GAAATAGTGTCTTTTCTCCAGAAAAATGCTTGTGAGAAATCATTTAAACATGTGACAA 65
Qy      2562 TTTAGAGATCTTTGTTTATTTTCACTGATTAATATATCTGCGCAATTAACAGAT 2618
Db      64 TTTAGAGATCTTTGTTTATTTTCACTGATTAATATATCTGCGCAATTAACAGAT 8

RESULT 6
CD557440
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

CD557440 894 bp mRNA linear EST 11-JUN-2003
AGENCOURT 14413568 NIH MGC 180 Homo sapiens cDNA clone
IMAGE:30387819 5', mRNA sequence.
CD557440
CD557440.1 GI:31583508
EST
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

```

National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: WGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM458 row: 1 column: 04
 High quality sequence stop: 610.
 Location/Qualifiers
 1. 894
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 /clone="IMAGE:30387819"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances) "
 /clone_lib="NIH MGC 180"
 /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
 Site 2: EcoRV (destroyed); Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.68 kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 Library."

FEATURES
 source
 1. 894

ORIGIN
 Query Match 28.08; Score 775.6; DB 14; Length 894;
 Best Local Similarity 97.18; Pred. No. 3.3e-135;
 Matches 799; Conservative 0; Mismatches 22; Indels 2; Gaps 1;
 645 TCAGTGTGTTGGCAGTTTCGTTGGATGAGGACTACCTAAATATGTTCTCAGTTTAA 704
 Db |
 6 TCAGTGTGTTGGCAGTTTCGTTGGATGAGGACTACCTAAATATGTTCTCAGTTTAA 55
 QY |
 705 CTGCAGAAACAGGGTAGAGGAGCGATCAATTTGACTTACTTTCCTGGTTCAFCGG 764
 Db |
 66 CTGCAGAAACAGGGTAGAGGAGCGATCAATTTGACTTACTTTCCTGGTTCAFCGG 125
 QY |
 765 TCATGATGCTGTTGCTGTTTCCTTATCATGTTGGGATGTTAGCATATTCGGAACG 824
 Db |
 126 TCAATGATGCTGTTGCTGTTTCCTTATCATGTTGGGATGTTAGCATATTCGGAACG 185
 QY |
 925 TGAAGAAATCTGTTGCTTCTTGCATGTGACTTTGGAAAGTTTGTCTGCAATTTCTGTG 884
 Db |
 186 TGAAGAAATCTGTTGCTTCTTGCATGTGACTTTGGAAAGTTTGTCTGCAATTTCTGTG 245
 QY |
 885 TAGAATCTGGCTGTGGGTTTGGACATATGACAGGAATTAATGTTCCAGTACAAATGTT 944
 Db |
 246 TAGAATCTGGCTGTGGGTTTGGACATATGACAGGAATTAATGTTCCAGTACAAATGTT 305
 QY |
 945 CAGATATGTTCACTTTGAAAGCCAGGATGACAAATATGCAATTAATGATATCGTTGGC 1004
 Db |
 306 CAGATATGTTCACTTTGAAAGCCAGGATGACAAATATGCAATTAATGATATCGTTGGC 365
 QY |
 1005 TTAATCATGCTGGAATTTTTCAGAGAGAGTTTAAGTCTGTGAGTAGTATATTTCA 1064
 Db |
 366 TTAATCATGCTGGAATTTTTCAGAGAGAGTTTAAGTCTGTGAGTAGTATATTTCA 425
 QY |
 1065 CTGACTGTGTTGAAATGACAGAGATGAGTCTGCCGCCAGATTCCTGCTGTGACAGAA 1124
 Db |
 426 CTGACTGTGTTGAAATGACAGAGATGAGTCTGCCGCCAGATTCCTGCTGTGACAGAA 485
 QY |
 1125 TCCAGAGATGTTCCAAACAGGCCCCAGGAGATCTCAGTACACCTTTATCAAGAGGGTT 1184
 Db |
 486 TCCAGAGATGTTCCAAACAGGCCCCAGGAGATCTCAGTACACCTTTATCAAGAGGGTT 545
 QY |
 1185 GTGGGAAGAAATGATTTCTTTTTCAGAGGAGCAACCACTGAGGCTGTGAGGTTTC 1244
 Db |
 546 GTGGGAAGAAATGATTTCTTTTTCAGAGGAGCAACCACTGAGGCTGTGAGGTTTC 605
 QY |
 1245 TGGGAATCTCCATTTGGGGTGACACAAATCTGGCCCATGATTTCTCACCATTACTCTGCTCT 1304

Db 606 TGGGAATCTCCATTTGGGGTGACACAAATCTGGCCCATGATTTCTCACCATTACTCTGCTCT 665
 QY 1305 GGGCTCTGTATTATGATAGAGGGAGCGGGGACAGACCAATGATGTCCTTGAGAGATG 1364
 Db 666 GGGCTCTGTATTATGATAGAGGGAGCGGGGACAGACCAATGATGTCCTTGAGAGATG 725
 QY 1365 ACAATCTCAGACCTGTCTATGTCCTCAGTAGAACTTTGAAACCAAGCCTG--TCAAG 1422
 Db 726 ACNACTCTCAGACCTGTCTATGTCCTCAGTAGAACTTTTAAACCCAGCGCGTCAAGA 785
 QY 1423 ATCTTTGAACACACATCCATGCGCAACAGCTTTTAATACACAC 1465
 Db 786 ATCTTTGAACACACATCCATGCGCAACACACCTTTTAATACCC 828

RESULT 7
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 LOCUS 831 bp mRNA linear EST 21-APR-2001
 DEFINITION RST38146 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG218523
 VERSION BG218523.1 GI:13744432
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (Bases 1 to 831)
 Harrington, J.J., Sherr, B., Rundlett, S., Jackson, P.D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
 Whittington, J., Lermer, L., Costanzo, D., McElligott, K., Booser, S.,
 Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cochran, K., Lo, K.,
 Offenbacher, J., Danzig, J., and Ducar, M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 11329013
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9536
 Email: scain@atersys.com
 High quality sequence stop: 509.
 Location/Qualifiers
 1. 831
 /Organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression
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 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

ORIGIN
 Query Match 27.58; Score 762.4; DB 12; Length 831;
 Best Local Similarity 97.08; Pred. No. 1e-132;
 Matches 798; Conservative 0; Mismatches 22; Indels 3; Gaps 2;
 1181 GGTGTGGGAGAAATGATTTCTTTTTCAGAGGAGCAACCACTGAGGTTGCTGAGG 1240
 Db 1 GTTAGTGGGAGAAATGATTTCTTTTTCAGAGGAGCAACCACTGAGGTTGCTGAGG 60
 QY 1241 TTTCTGGGAATCTCCATTTGGGGTGACACAAATCTCGGCATGATTTCTCACCATTACTCTG 1300
 Db 61 TTTCTGGGAATCTCCATTTGGGGTGACACAAATCTCGGCATGATTTCTCACCATTACTCTG 120
 QY 1301 CTCTGGGCTCTGATTATGATAGAGGGAGCGGGGACAGACCAATGATGTCCTTGAAG 1360

Db 121 CTCTGGGCTCTGTATTATGATAGAGGAGCGCTGGACACAGCAAAATGATGTCCTTGAAG 180

QY 1361 AATGACAACCTCTCAGCACCTGTCTCCTCAGTAGAAGCTGTGAAACCAAGCCTGTCA 1420

Db 181 AATGACAACCTCTCAGCACCTGTCTCCTCAGTAGAAGCTGTGAAACCAAGCCTGTCA 240

QY 1421 AGAATCTTTGAAACACACATCCATGCGCAAAAGCAGCTTTAAATACACACCTTTGAGATGGAGGAG 1480

Db 241 AGAATCTTTGAAACACACATCCATGCGCAAAAGCAGCTTTAAATACACACCTTTGAGATGGAGGAG 300

QY 1481 TTATAAAAGAAATGTACAGAGAAACCAACAACTTTGTTTACTGGACTGTGAATTT 1540

Db 301 TTATAAAAGAAATGTACAGAGAAACCAACAACTTTGTTTACTGGACTGTGAATTT 360

QY 1541 TTGAGTACATCTATGTTTTCAGAAATGTAGAAATATAAAATGTTTGCATATAAATAAC 1600

Db 361 TTGAGTACATCTATGTTTTCAGAAATGTAGAAATATAAAATGTTTGCATATAAATAAC 420

QY 1601 ACTTAAGCATATCTATCTATGCTTTAAATGAGGATGGAAAGTTTTCATGTCAATAGT 1660

Db 421 ACTTAAGCATATCTATCTATGCTTTAAATGAGGATGGAAAGTTTTCATGTCAATAGT 480

QY 1661 CACCACTGACATATCTATGCTTTAAATGAGGATGGAAAGTTTTCATGTCAATAGT 1720

Db 481 CACCACTGACATATCTATGCTTTAAATGAGGATGGAAAGTTTTCATGTCAATAGT 540

QY 1721 GTAGCCTGTGTATGACTTTTACTGAACACAGTTTATGTTTGGGCGAGCATGTTTGATTA 1780

Db 541 GTAGCCTGTGTATGACTTTTACTGAACACAGTTTATGTTTGGGCGAGCATGTTTGATTA 600

QY 1781 GCATTCGGATCCATGCAACAGATCACATATGTTGGGACTGGCCATAGTAAAGGTT 1840

Db 601 GCATTCGGATCCATGCAACAGATCACATATGTTGGGACTGGCCATAGTAAAGGTT 660

QY 1841 GATTACTTCTACCACTAGTATATAAAGTACTAA-TTAAATGCTAACATAGGAAGTTAG 1899

Db 661 GTTTTACTTCTACCACTAGTATATAAAGTACTAA-TTAAATGCTAACATAGGAAGTTAG 720

QY 1900 AAAATACATAAATTTTATCTACGCGATCTATCTTCTGATGCTAAATAATATAT 1959

Db 721 AAAATACATAAATTTTATCTACGCGATCTATCTTCTGATGCTAAATAATATAT 780

QY 1960 ATCAGAAAACCTTCAATATTTGGTACCTACCTAAATGATTTT 2002

Db 781 ATC--AAAACTTTTCATAAAGGTGACTACCTAAATAGGATTTT 821

RESULT 8

BF338835

LOCUS 62036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321

DEFINITION 5', mRNA sequence.

ACCESSION BF338835

VERSION BF338835.1 GI:11285254

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabp-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov.

Plate: LIAM9501 row: p column: 18

High quality sequence stop: 735.

Location/Qualifiers

1. 926

/organism="Homo sapiens"

/mol_type="mRNA"

/cd_xref="taxon:9606"

/clone="IMAGE:4184321"

/lab_host="DH10B (T1 phage-resistant)"

/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 27.4%; Score 758.6; DB 10; Length 926;

Best Local Similarity 96.1%; Pred. No. 5e-132;

Matches 798; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

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Db 1 GAGATTCCTCCAGGATGTTCCAAACAGGCCACCCAGGAGATCTCAGTGACCTTTATCAAG 60

QY 1179 AGGGTTGGGAAGAAATGATTCTCTTTTGGAGGAAACCAACAACTGCAGGTCTGA 1238

Db 61 AGGGTTGGGAAGAAATGATTCTCTTTTGGAGGAAACCAACAACTGCAGGTCTGA 120

QY 1239 GGTTCCTGGGAATCTCCATTTGGGTTGACACAAATCTCGCCATGATTCCTCATTATCTC 1299

Db 121 GGTTCCTGGGAATCTCCATTTGGGTTGACACAAATCTCGCCATGATTCCTCATTATCTC 180

QY 1299 TGCTCTGGGCTCTGTATTATGATAGAGGAGCGGGACAGACCAAAATGATGCTCTTGA 1358

Db 181 TGCTCTGGGCTCTGTATTATGATAGAGGAGCGGGACAGACCAAAATGATGCTCTTGA 240

QY 1359 AGAATGACAACTCTCAGCACCTGTCTATGTCCTCAGTAGAAGCTGTGAAACCAAGCCTGT 1418

Db 241 AGAATGACAACTCTCAGCACCTGTCTATGTCCTCAGTAGAAGCTGTGAAACCAAGCCTGT 300

QY 1419 CAAGAATCTTTGAAACACACATCCATGCGCAAAAGCAGCTTTAAATACACACTTTGAGATGGAGG 1478

Db 301 CAAGAATCTTTGAAACACACATCCATGCGCAAAAGCAGCTTTAAATACACACTTTGAGATGGAGG 360

QY 1479 AGTTATAAAAGAAATGTACAGAGAAACCAACAACTTTGTTTACTGGACTTGTGAAT 1538

Db 361 AGTTATAAAAGAAATGTACAGAGAAACCAACAACTTTGTTTACTGGACTTGTGAAT 420

QY 1539 TTTTGAGTACATATCTATGTTTTCAGAAATATGTAGAAATAAAATGTGCCATAAATA 1598

Db 421 TTTTGAGTACATATCTATGTTTTCAGAAATATGTAGAAATAAAATGTGCCATAAATA 480

QY 1599 ACACCTTAGCATATCTATCTGCTTTAAATGAGGATGGAAAGTTTTCATGTCATAA 1658

Db 481 ACACCTTAGCATATCTATCTGCTTTAAATGAGGATGGAAAGTTTTCATGTCATAA 540

QY 1659 GTCCACCATCGACAAATAATGATGCCCTTAAATGCTCAAGACAGATGTCTATCCACT 1718

Db 541 GTCCACCATCGACAAATAATGATGCCCTTAAATGCTCAAGACAGATGTCTATCCACT 600

QY 1719 GTGTAGCCTGTGTATGACTTTTACTGAACACAGTTTATGTTTGGGCGAGCATGTTTGAAT 1778

Db 601 GTGTAGCCTGTGTATGACTTTTACTGAACACAGTTTATGTTTGGGCGAGCATGTTTGAAT 659

QY 1779 TAGCATTTCCGCATCCATGCAAAAGTACATATGTTGGGACTGGAGCATAGTAAAGG 1838

Db 660 TAGCATTTCCGCATCCATGCAAAAGTACATATGTTGGGACTGGAGCATAGTAAAGG 719

QY 1839 TTGATTACTTCTACCACTAGTATATAAAGTACTAA-TTAAATGCTAACATAGGAAGTTA 1898

Db 720 TTGATTACTTCTACCACTAGTATATAAAGTACTAA-TTAAATGCTAACATAGGAAGTTA 778

QY 1899 GAAATATCTATTAATCTTATTACTCAGCGATCTATTCTTCTGATCTAA 1948
 Db 779 GAAATATCTATTAATCTTATTACTCAGCGATCTATTCTTCTGATCTAA 828

RESULT 9

CD656678

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

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CD656678 783 bp mRNA linear EST 18-JUN-2003
 AGENCOURT_14556073 NIA Human H1 Embryonic Stem Cell cDNA Library
 (Long) Homo sapiens cDNA clone IMAGE:30427246 5', mRNA sequence.
 CD656678
 CD656678.1 GI:31897214
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (Bases 1 to 783)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm.0A07 Bethesda, MD 20892
 Email: gmapbs-i@mail.nih.gov
 Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
 cDNA Library Preparation: Yulan Piao and Minoru Ko
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC c lone distribution information
 can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM514 row: f column: 23
 High quality sequence stop: 724.

FEATURES

source

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 /db_xref="taxon:9606"
 /clone="IMAGE:30427246"
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
 (Long)"
 /notes="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;
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 Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01/
 cell line. Undifferentiated human ES cell line WA01/H1
 was obtained from Wicell Research Institute, Inc.,
 Madison, WI, cultured according to their instructions, on
 MEF feeders. They formed round colonies with defined edges
 and were positive for alkaline phosphatase, SSEA-4, OCT3,
 OCT4, REX1, UTE, TERT, SOX2, CX43 and CX45. They are
 negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLK1, SSEA-1,
 TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days
 after plating), the ES cells from 4 X 6 cm dishes were
 treated with 1 mg/ml collagenase, type IV
 (Invitrogen/Gibco) for 5-10 min and gently scraped off
 with 5 ml pipette. RNA was purified with Trizol Reagent
 from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558
 (2001). [PMID:11544199] Double-stranded cDNAs were
 synthesized with an Oligo(dT) primer [Invitrogen:
 5'-pGACTAGTCTAGATCCGAGCGCGCCCTTTTCTTTTCTTTT-3'] from
 3.4g of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to Loxe-linker LL-Sal4, purified by phenol/chloroform
 extraction, and separated from free linkers by
 Centricon-100 column. Then, the cDNAs were amplified by
 long-range high fidelity PCR using Ex Taq polymerase
 (Takara) with a primer Sal4-S for 25 cycles. The products
 were purified by phenol/chloroform extraction and

Centricon-100 column. The cDNAs were digested with SalI
 and NotI enzymes and cloned into SalI/NotI site of
 pCMV-Sport6 plasmid vector. The average insert size is
 about 3.6kb."

ORIGIN

Query Match 26.4%; Score 731.6; DB 14; Length 783;
 Best Local Similarity 98.3%; Pred. No. 6.1e-127; Indels 2;
 Matches 760; Conservative 0; Mismatches 10;
 QY 1182 GTTGTGGGAAGAAATGATTCTCTTTTGTAGAGGAACCAAAACAACCTGCTGAGGT 1241
 Db 3 GTAAATCCGAAGAAATGATTCTCTTTTGTAGAGGAACCAAAACAACCTGCTGAGGT 62
 QY 1242 TTCTGGGAATCTCCATTTGGGGTGACACAAATCCTGGCCATGATCTCACCATTACTTGC 1301
 Db 63 TTCTGGGAATCTCCATTTGGGGTGACACAAATCCTGGCCATGATCTCACCATTACTTGC 122
 QY 1302 TCTGGCTCTCTGATTATGATAGAGGGAGCGGGGACAGACCAAAATGATGCTCTTGAAGA 1361
 Db 123 TCTGGCTCTCTGATTATGATAGAGGGAGCGGGGACAGACCAAAATGATGCTCTTGAAGA 182
 QY 1362 ATGACAACTCTCAGACCTGTCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 1421
 Db 183 ATGACAACTCTCAGACCTGTCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 242
 QY 1422 GAATCTTTGAACACACATCCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 1481
 Db 243 GAATCTTTGAACACACATCCATGTCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 302
 QY 1482 TATAAAGAAATGTCACAGAGAAAAACCAAACTTTTACTGGACTTGTGAATTTT 1541
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 Db 363 TGACTACATCTATGCTTTTTCAGAAATATGTAGAAATATAAATGTTGCCATAAATAACA 422
 QY 1602 CCTAAGCATATATCTATGCTTTTAAATGAGGATGGAAGATTTTCATGTCATAGTC 1661
 Db 423 CCTAAGCATATATCTATGCTTTTAAATGAGGATGGAAGATTTTCATGTCATAGTC 482
 QY 1662 ACCACCTGGACATATATGATGCTTTAAATGCTGAGACAGATGTCATACCCACTGTG 1721
 Db 483 ACCACCTGGACATATATGATGCTTTAAATGCTGAGACAGATGTCATACCCACTGTG 542
 QY 1722 TAGCTGTGTATGACTTTTACTGAACACAGTTATGTTTTCAGGCAGCATGTTGATTAG 1781
 Db 543 TAGCTGTGTATGACTTTTACTGAACACAGTTATGTTTTCAGGCAGCATGTTGATTAG 602
 QY 1782 CATTTCCGCATCCATGCAAAACGAGTCACATATGTTGGGAGTGGAGCCATAGTAAAGTTG 1841
 Db 603 CATTTCCGCATCCATGCAAAACGAGTCACATATGTTGGGAGTGGAGCCATAGTAAAGTTG 662
 QY 1842 ATTTTACTTCTACCAACTAGTATATAAGTACTTAATTAATGCTTAACATAGGAAGTTAGA 1901
 Db 663 ATTTTACTTCTACCAACTAGTATATAAGTACTTAATTAATGCTTAACATAGGAAGTTAGA 722
 QY 1902 AATACTAATACTTTTATTACTCAGGCATCTATTCTTCTGATCCTAAATAAAT 1954
 Db 723 AATACTA--TAACTTTTATCTCAGGCATCTATTCTTCTGATCCTAAATAAAT 772

RESULT 10

AY416018

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AY416018 918 bp DNA linear GSS 12-DEC-2003
 Mus musculus HCM5750 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 AY416018
 AY416018.1 GI:39771978
 GSS.
 Mus musculus (house mouse)
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 918)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
JOURNAL
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Matches 759; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
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DB 1 ATGCCAGAGAGATTCGGTGAAGTCTGGCTGCTGGCTGCTACGCCCTCAATCTGCTC 60
QY 629 TTTTGGTTAATGTCATCAGTCTGCTGGCAGTTCTGCTGGATGAGGAGTACCTAAAT 698
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DB 121 AATGTTCTCACTTTAATGTCAGAAACGAGGATGAGGAGGAGTCACTTTGACTTACTTT 180
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UI-CF-EC1-adx-p-17-0-UI 3', mRNA sequence.
BU688134
BU688134.1 GI:23544635
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 703)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
9704477
PUBMED
8889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.
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QY      1661 CACACCTGACAAATATGATGATCCCTTAAATGCTGAAGACAGATGTATACCCCACTGT 1720
Db      481 CACACCTGACAAATATGATGATCCCTTAAATGCTGAAGACAGATGTATACCCCACTGT 540
QY      1721 GTAGCCTGTATGATCTTTTACTGAACACAGTATGTTTGTAGGACGATGTTTGATTA 1780
Db      541 GTAGCCTGTATGATCTTTTACTGAACACAGTATGTTTGTAGGACGATGTTTGATTA 600
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Db      601 GCATTTCCGATCCATGCAACAGTACACATATGTTGGAGCTGAGCCATAGTAAAGGTT 660
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Db      661 GGATTAATCTTCTACCCCACTATATTTAAAGGTCCTAATTAATGCTAAACATAGGAAGTT 720
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LOCUS DXFZp686p15255_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DXFZp686p15255 5', mRNA sequence.
ACCESSION BX487248
VERSION BX487248
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 700)
AUTHORS Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M. and Wiemann S.
EBO (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)

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TITLE Unpublished (2003)
JOURNAL Contact: MIPS
COMMENT Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686p15255) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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Best Local Similarity 99.1%; Pred. No. 9e-118;
Matches 695; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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VERSION AY416017.1 GI:39771977
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)

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ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 918)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

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TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 918)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

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Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

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 QY 929 GTTCCAGTAAATGGTCAGATATGCTCACTTGAAGCCAGGATGACAAATATGGAATTA 988
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Db 781 ATGTCCTTGAGAAATGACAACTCTCAGACCTGTCATGTCCTCAGTAGAATCTGTTGAA 840
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 Db 901 GAGATGGAGGAGTTATAA 918

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 VERSION
 BG538289.1 GI:13530521
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 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 826)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."

ORIGIN
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 Best Local Similarity 94.3%; Pred. No. 3.5e-110;
 Matches 742; Conservative 0; Mismatches 38; Indels 7; Gaps 7;

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 Db 61 CTAAACATTTGCTTAAAGCTGATCAGGATTTTGTATATAAGTCTGTGTTAAATCTGT 120
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Db 121 ATATTTCAGTCGATTTTCAGTTCGTGATAATGTTAAGAAATACCAATTATGAAAGGAAAAATT 190
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Db 181 TGTCTCTGTATAGCATCATTTATTTTTCAGCTTTCCTGTTAATAAAGCTTTTACATTTCTGTC 240
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Db 361 TAAGAAATTTGCACATATACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTCTCCC 420
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Db 421 AAATGAAGACTCTTTTTGACACTAAACACTTTTTAAACAAAGCTTATCTTTGCTTTCTCCA 480
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Db 776 TAAAAA 782

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.6	2.0	11049	US-10-204-708-22	Sequence 22, Appl
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3	51.6	1.9	3095	6 5231168-1	Patent No. 5231168
4	51	1.8	8093	US-10-204-708-31	Sequence 31, Appl
5	51	1.8	640681	US-09-790-988-1	Sequence 1, Appl
6	50.8	1.8	1884	US-09-468-265-4	Sequence 4, Appl
7	49.6	1.8	11050	US-10-204-708-86	Sequence 86, Appl
8	49	1.8	724	US-08-998-416-683	Sequence 683, Appl
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13	48.8	1.8	8654	US-08-921-177-6	Sequence 6, Appl
14	48.8	1.8	8654	US-08-362-577C-6	Sequence 6, Appl
15	48.8	1.8	8654	US-08-920-828-6	Sequence 6, Appl
16	48.4	1.7	3600	US-08-894-731-1	Sequence 1, Appl
17	48	1.7	7786	US-09-790-988-2	Sequence 2, Appl
18	48	1.7	19233	US-10-204-708-46	Sequence 46, Appl
19	47.8	1.7	837	US-08-998-416-288	Sequence 288, Appl
20	47.6	1.7	854	US-08-998-416-534	Sequence 534, Appl
21	47.6	1.7	19124	US-08-487-826B-13	Sequence 13, Appl
22	47.2	1.7	832	US-09-621-976-2813	Sequence 2813, Appl
23	47.2	1.7	6113	US-10-204-708-14	Sequence 14, Appl
24	46.6	1.7	2058	US-08-749-391-1	Sequence 1, Appl
25	46.6	1.7	2058	US-09-390-200-1	Sequence 1, Appl
26	46.2	1.7	8951	US-10-204-708-80	Sequence 80, Appl
27	45.8	1.7	19124	US-08-487-826B-13	Sequence 13, Appl

28	45.6	1.6	636	3	US-08-998-416-1137	Sequence 1137, Appl
29	45.6	1.6	3001	4	US-09-539-333D-204	Sequence 204, Appl
30	45.6	1.6	6265	4	US-09-129-112-3	Sequence 3, Appl
31	45.6	1.6	10467	4	US-10-204-708-2	Sequence 2, Appl
32	45.6	1.6	20674	4	US-09-641-638-651	Sequence 651, Appl
33	45.6	1.6	8961	4	US-10-204-708-80	Sequence 80, Appl
34	45.2	1.6	5152	4	US-10-204-708-73	Sequence 73, Appl
35	45	1.6	827	3	US-08-998-416-535	Sequence 535, Appl
36	45	1.6	4673	1	US-07-638-431-1	Sequence 1, Appl
37	45	1.6	4673	5	PCT-US92-00018-1	Sequence 1, Appl
38	45	1.6	6070	4	US-10-204-708-10	Sequence 10, Appl
39	45	1.6	6182	4	US-10-204-708-87	Sequence 87, Appl
40	45	1.6	6317	4	US-10-204-708-11	Sequence 11, Appl
41	45	1.6	10640	4	US-09-417-485D-5	Sequence 5, Appl
42	44.6	1.6	732	3	US-08-998-416-1036	Sequence 1036, Appl
43	44.4	1.6	10467	4	US-10-204-708-1	Sequence 1, Appl
44	44.2	1.6	860	3	US-08-998-416-287	Sequence 287, Appl
45	44	1.6	6265	4	US-09-129-112-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-204-708-22
; Sequence 22, Application US/10204708
; Patent No. 667731
; GENERAL INFORMATION:
; APPLICANT: PLEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: By Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 22
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-22

Query Match	2.0%	Score 55.6	DB 4	Length 11049
Best Local Similarity	55.8%	Pred. No. 0.00015		
Matches 106	Conservative 0	Mismatches 84	Indels 0	Gaps 0
QY	2541	AATCAATAAATGTCAGATTTAGAGATCTTTGTTTATTTTACCTGATTAATAACT	2600	
Db	9819	ATTTTAAATTTTATTAAGTAGATTTATTTTATTTTATTTTATTAATGAGAAATA	9878	
QY	2601	GTGGCAATTTACAGATTTATTAATTTTACAGAGTAGTATTTATTTTGAAT	2660	
Db	9879	GGTATAGAAAATAAATTTATTTTATTTTATTTATTTATTTAGTGATAGTTGTAA	9938	
QY	2661	GGGAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTCTCAGAAATATGGAAGA	2720	
Db	9939	GTGTAGAGTTAGTATTTGAAATTTTATTTATTTATTTATTTATTTAGAGTTGTAAGA	9998	
QY	2721	AAATTAAT 2730		

Db 9999 AATTAAATAT 10008

RESULT 2

US-09-790-988-1

Sequence 1, Application US/09790988

Patent No. 6632935

GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI

APPLICANT: WATANABE, HIDEMI

APPLICANT: HATTORI, MASAHIRA

APPLICANT: SAKAKI, YOSHIYUKI

TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REFERENCE: 081356/0159

CURRENT APPLICATION NUMBER: US/09/790, 988

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: JP2000-107160

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 640681

TYPE: DNA

ORGANISM: Buchnera sp.

US-09-790-988-1

Query Match 2.0%; Score 54.8; DB 4; Length 640681;

Best Local Similarity 47.6%; Pred. No. 0.0042;

Matches 233; Conservative 0; Mismatches 247; Indels 10; Gaps 2;

Qy 2235 TACACATATAACTGTATTATTAATACCTAACCACTAATTTTGAATATACCAGTGTGATA 2294

Db 353270 TAAATAAATAGTTTTATTAAATCTTTATCATATATTTTTTAAAT-----AGAAATAC 353323

Qy 2295 CATAGGATCATTTTACAGATGTAGTCGGTCTTTAGGAGTATTAAAGAAATTTG 2354

Db 353324 CTTTAAATAATATGATACATACGAAATAATTTCTTTAATTTTTTTTATATATTNAATT 353383

Qy 2355 CACATAACTTAGTTGATTCAGAAAGACCTGTATGCTTTTTTCTCCCAATGAAGACTC 2414

Db 353384 ATTAATAATATGCAATTCATTCGTAATTTGATTTCTTTATTCATACCTATTGTTAGTT 353443

Qy 2415 TTTTGACATCAACACTTTTAAAGCTTCTTTGCTTCCTCCCAACAGAACCAAT 2474

Db 353444 TTTAAATAATAAAGAAATTTTATAAATAATTTATCTATTTTATAGAAATACATAAAT 353503

Qy 2475 AGTCTCCAAGTCAATATAAATTC---TACAGAAATAGTGTCTTTTCTCCAGAAAAA 2530

Db 353504 TTTTAAATATTTACTTAAATTCATATTACTTTAAATAATTTTATTTTATTAGAAAT 353563

Qy 2531 TGCTGTGAGAACTATTAAACATGTGCAATTTAGAGATCTCTGTTTATTCTGCTGA 2590

Db 353564 AACATTAAATGATGATACATTTTGAATTTAAATTAATAATCAACATAAATTTTCTGA 353623

Qy 2591 TTAATATACGTGCAAAATTTACAGATTTATTAATTTTTTTTACAGAGTATAGTATATT 2650

Db 353624 TTTTAAATAAATATATCAAGAAATAATACAAATTTTAAATAATTTTGAATTA 353683

Qy 2651 TATTGAAATGGGAAAGTGCATTTTACTGATTTTGTGATTTTCTGATTTCTCAGAA 2710

Db 353684 TATTATTAAATGGTAATCTCCCTTTTATTTATTAATAATTTCTTTTTCATTTGAAAT 353743

Qy 2711 TAAGGAAAGA 2720

Db 353744 TATAGAAAGA 353753

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/409,658

FILING DATE: 18-SEP-1989

SEQ ID NO:1:

LENGTH: 3095

5231168-1

Query Match 1.9%; Score 51.6; DB 6; Length 3095;

Best Local Similarity 45.7%; Pred. No. 0.00075;

Matches 341; Conservative 0; Mismatches 389; Indels 16; Gaps 4;

Qy 2014 AAAATATTTCTTACCACCTTAAAGAGCAAGCTAACACATTTCTTTAGCTCATCAGGATT 2073

Db 2332 ATATTTTCCAAAAACATTTAAATAATTAACAAAAAATAAATAAATAAATAAATAAATAA 2391

Qy 2074 TTTTGTATATAGTCTCTGTGTTAAATCTGTATATTCAGTTCAGTTCTGATATGT 2133

Db 2392 TATTAAATAAATAATTTTTTTCTTATATATGTAACATAATTTTATTATTAATAATATAT 2451

Qy 2134 TAAGATTAACCATTTATGAAAAAGGAAAAATTTGCTGTATAGCATCAATTTTTCAGCCTT 2193

Db 2452 ATATTATATAAAGAATACTAGGATTTCTGTATATAAGAAATAAATTCATTGTATATTA 2511

Qy 2194 TCCTGTTAATAAGCTTTTACTATTTCTGCTCTGGCTTATATTACATATACATATACCTGTTATT 2253

Db 2512 TTATAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2571

Qy 2254 TAAATACCTTAA---CCACTAATTTTGAATAATACCAGTGTGATACATAGGAATCAATTTATT 2310

Db 2572 ATAATAATAAATAATATAGAAACATTTACAGTATATTTTATAAATCTGAAGTATACATGTA 2631

Qy 2311 CAGAAATGTAGTCTGGTCTTTAGGAAGTATTAAATAAGAAAAATTTGCAATCAATCTAGTTGA 2370

Db 2632 ATAAAAAATTTTCTGGCTTTATAATAATAAATAAATAAATAAATAAATAAATAAATAAATA 2691

Qy 2371 TTCAGAAAGGACTTTGATGCTGTTTCTCCCAATGAAGACTCTTTTTCACACTAAACA 2430

Db 2692 TTAAGAAATATTTATATAATATGATTAATAATAATAATAATAATAATAATAATAATAATA 2741

Qy 2431 CTTTAAAAAGCTTATCTTTTGGCTTCTCCAAACAGAACCAATAGTCTCCAAAGTCAATA 2490

Db 2742 TTTTATTTATCATTTTTCATAAATAATTTATAAATAATAATAATAATAATAATAATAATA 2801

Qy 2491 TAAATCTACAGAAAAATAGTCTCTTTTCTCCAGAAAAATGCTTTGTGAGATC--ATTA 2548

Db 2802 TAAATATTTATGATATATTTTATATATATATATATATATATATATATATATATATATAT 2861

Qy 2549 AAACATGTGCAAAATTTAGAGATCTTTTGTGTTTAT--TTCACTGATTAATAATACTGTGCA 2607

Db 2862 AAATATGAACAATAAATCTATGTTCTGATTTTATATTTCTTAGGTAAATAAATTCATATAT 2921

Qy 2608 ATTACACAGATTTAAATTTTTCAGAGTATAGTATATTTTATTGAAATGGGAAA 2667

Db 2922 ATTTTATTTTAAATAATTTTAAACCAATGATATAATAAATAAATAAATAAATAAATAA 2981

Qy 2668 GTGCAATTTTACTGATTTTGTGTTTATTTTCTCAGAAATGGAAGAAAAATTA 2727

Db 2982 GTAAGATTTTATATGTCCTCAATAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3041

Qy 2728 AATGTGCAATAAATAATTTTCTAGAG 2753

Db 3042 TATATATTATTAGTTATATTATATAG 3067

RESULT 3

5231168-1

Patent No. 5231168

APPLICANT: DIEBIELE, MORTEN; BORRE, MARTIN; JENSEN, SOREN;

VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.

TITLE OF INVENTION: MALARIA ANTIGEN

RESULT 4

US-10-204-708-31

Sequence 31, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENROCK, Christian

APPLICANT: BERLIN, Kurt

;; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;; TITLE OF INVENTION: by Assessing DNA Methylation
;; FILE REFERENCE: 5013.1012
;; CURRENT APPLICATION NUMBER: US/10/204,708
;; PRIOR FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: PCT/EP01/03971
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: DE 10019058.8
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: DE 10019173.8
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: DE 10032529.7
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: DE 10043826.1
;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 31
;; LENGTH: 8093
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-31

Query Match 1.8%; Score 51; DB 4; Length 8093;
Best Local Similarity 43.0%; Pred. No. 0.0023;
Matches 249; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 2147 TATGAAGGAAATTTGCTCTATAGCATCATTTTCTAGCTTTCTCTGTAATAA 2206
DB 513 TAGTAAGGTTAAATTTAAATTTTGGTTTATTTTATTTTAAATGATTAAG 572

QY 2207 GCTTTACTATCTGCTCGGCTTATATTACATATACTGTATTAAATCACTTAAC 2266
DB 573 ATGTAAATTAATTTTATTAATTTTAAAGTAAATATATTGGAATTTTATAAATGATA 632

QY 2267 ACTAATTTGAAATTTACAGTGTGATACATAGGATCATTTTACAGATGAGTCTGT 2326
DB 633 AGATTTTAAATTTAAAGGAATGGGCTTAGAAGTAGAAGTGGTTTATAGTTTATG 692

QY 2327 CTTTAGAGATTAATAAGAAATTTGCACATACTTGTGATTCAGAAAGGACTGT 2386
DB 693 TTTTATTTTAAAGTAAATAGTTTGTGTGAATTTTAAAGTTATTTGGGAATTTATCGT 752

QY 2387 ATGCTGTTTCTCCAAATGAAGACTCTTTTGTGACACTAAACACTTTTAAAGCTTA 2446
DB 753 AGATTTTGTGTTTCTTTTTCGGTTTATTTATGTTTGTGTTTATGATATGTAAGTT 812

QY 2447 TCTTTGCTTCTCCAAAGAGCAATAGTCTCCAAAGCAATATAAATTTACAGAAA 2506
DB 813 TATTTTAAATTAATTTTATGTTTGTGATTTTATGATATGATTTTATCGATATGTA 872

QY 2507 TAGTGTCTTTTCTCCAGAAAATGCTTTGTGAGATCAATTAACACATGTGCAATTTAG 2566
DB 873 TTTTATTTTGTGTTTAAATATGATTAATAGGATAGAGTTTAAATTTGATTAATTT 932

QY 2567 AGATTTCTTTTATTTTCTACTGATTAATATAGTCTGGCAATTTACAGATTTAAT 2626
DB 933 AATTTTGAATTAATAGTGTATGGTGAATTAATGAAATTTATTAATGTTTATGAT 992

QY 2627 TTTTTCACAGATGATAGTATATTTTAAATTTGAAATGGAAAGTGCATTTTACTGTATTT 2686
DB 993 TTTTATGTTAAATTTAGAGGTTGGAATTTTATTTTATTTAGTATTTTGTAGTTT 1052

QY 2687 GTGATTTTCTTTTCTCAGAAATATGGAAGAAATTT 2725
DB 1053 GTTAGTTTCTATTTTAAATTTTGTGTTTAAATGTTAATTT 1091

RESULT 5
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935

;; GENERAL INFORMATION:
;; APPLICANT: SHIGENOBU, SHUJI
;; APPLICANT: WATANABE, HIDEMI
;; APPLICANT: HATORI, MASAHIRA
;; APPLICANT: SAKAKI, YOSHIYUKI
;; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
;; FILE REFERENCE: 081356/0159
;; CURRENT APPLICATION NUMBER: US/09/790,988
;; CURRENT FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: JP2000-107160
;; PRIOR FILING DATE: 2000-04-07
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 640681
;; TYPE: DNA
;; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 1.8%; Score 51; DB 4; Length 640681;
Best Local Similarity 44.4%; Pred. No. 0.049;
Matches 338; Conservative 0; Mismatches 415; Indels 8; Gaps 3;

QY 1907 TAATAACTTTTACTCAGCGATCTATTTCTCTGATGCTAAATAAATTAATATATCAGAA 1966
DB 518397 TTATATTTTCTATTTTAAATAATGTTTATATATCTTAAGTATAATTTTATAA 518338

QY 1967 AACTTTCAATATTTGGTGACTACTACCTAAATGTGATTTTCTGCTGGTTACTAAAAATTTCT 2023
DB 518337 AAATATATGATTTATGATCATAAATTTTGAATTAATTCATAAATAATTTTATTTT 518278

QY 2024 TACCACTTAAAGAGAGCTAACACATTTGCTTAACTGATCAGGATTTTTTGTATAT 2083
DB 518277 ACACACTTAACTACTAGTCTTTTAAAGTTTTTATCTTTCCATTCATTTAAATGTGTA 518218

QY 2084 AAGCTGTGTTAAATCTGTATAATTCAGTCGATTTCTGATTAATTTTAAAGAACTAA 2143
DB 518217 GTATTTAAGTTAAGATATATTTTCTATCATTTTGTATGATTTGAAATTTTAAAT 518158

QY 2144 CATATGAAAAAGGAAATTTGCTGCTGATAGCATCATTTATTTTGTAGCTTTTCTGTTAAT 2203
DB 518157 ATTCGGTCTATTAAATAGCGTTTGATTAATAAATCATCGCTAAATAAATTTATTTCT 518098

QY 2204 AAGCTTTTACTATTTCTCTCGGCTTATATACATATACTGTTTATTTTAAATACTTA 2263
DB 518097 AAATGTGTAAGACCTTTTATAGATTAATGATGAAATTTGGCTATCGTCATAAATTTCA 518038

QY 2264 ACCCTAATTTGAAATTTACAGTGTGATACATAGGAATCATTTATTCAGAAATGTAGTCT 2323
DB 518037 AATTTTATTTT--ATTTAGATATTAATAATTTTATTTTCTAGAGTCATTAATTT 517980

QY 2324 GGTCTTTAGGAAGTATTAATAAGAAATTTGCACATACTTAGTTGATTCAGAAAGGACT 2383
DB 517979 GATATATGTCCTTTTATTAATAAAAAAATAGATAAATTTTATGCTATTTTGTAT 517920

QY 2384 TGTATGCTGTTTTTCTCCAAATGAAGACTCTTTTGCACACTAAACACTTTTTTAAAAAGC 2443
DB 517919 AGTATATATTTGATTTTGTATTAATAATTTTAAAAAATGTAATTTTATTTTAA 517860

QY 2444 TTATCTTTGCTCTCCAAACAGAGCAATAGTCTCCAGTCAATATAAATTTTACAGA 2503
DB 517859 AATTTTAACAATTTTAAAAAATAATTTCAATTTTTCACAGATTTACTTTTTTATAAGA 517800

QY 2504 AAATAGTCTCTTTTCTCCAGAAATGCTTTGTGAGATCATTTAAACATGTCGACATTT 2563
DB 517799 TAATAAATTTTCTATAAATAATTTTGTATAATAAGATTAATTAAGATTTTGTG--AAT 517743

QY 2564 TAGGATTTCTTTTATTTTCTACTGATTAATACTGTGGCAATTTACAGATTTAATA 2623
DB 517742 AAAAAATACATTTTATTTTGTAGGTTTTTGAATGATTTTTTAACTATAATAATTTTGA 517683

QY 2624 AATTTTTTCAAGAGTATAGTATATTTTATTTGAAATGGGA 2664

Db 517682 AACATTATCATGATTAATTAATATTTTTTTTCTGAAATGGA 517642

RESULT 6

US-09-468-265-4/c

; Sequence 4, Application US/09468265

; Patent No. 6379928

; GENERAL INFORMATION:

; APPLICANT: Berka, Randy M

; APPLICANT: Cullen, Daniel

; APPLICANT: Gray, Gregory L

; APPLICANT: Hayenga, Kirk J

; APPLICANT: Lawlis, Virgil B

; TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Process

; TITLE OF INVENTION: Making Same and Vectors for Making Same

; FILE REFERENCE: A-42909-5

; CURRENT APPLICATION NUMBER: US/09/468, 265

; CURRENT FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 08/484,384

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/284,942

; PRIOR FILING DATE: 1994-08-02

; PRIOR APPLICATION NUMBER: 07/413,010

; PRIOR FILING DATE: 1989-09-25

; PRIOR APPLICATION NUMBER: 07/163,219

; PRIOR FILING DATE: 1988-02-26

; PRIOR APPLICATION NUMBER: 06/882,224

; PRIOR FILING DATE: 1986-07-07

; PRIOR APPLICATION NUMBER: 06/771,374

; PRIOR FILING DATE: 1985-08-29

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patent version 3.1

; SEQ ID NO 4

; LENGTH: 1864

; TYPE: DNA

; ORGANISM: Emericella nidulans

US-09-468-265-4

Query Match 1.8%; Score 50.8; DB 4; Length 1864;

Best Local Similarity 44.3%; Pred. No. 0.00093;

Matches 411; Conservative 0; Mismatches 492; Indels 25; Gaps 4;

QY 1842 ATTACTCTTCCCACTAGTATATTAAGTAACTAAATGCTTAACATAGGAAGTTGAA 1901

Db 1614 AATTAGAAATTAATAAATATCTCTAGATAATTAATAATTTAGAAAATAGATAT 1555

QY 1902 AATCTAATAAATCTTTTATTTACTCAGCGATCTATCTTCTGATGCTAAATAATATATAT 1961

Db 1554 AATTGTAATCTCTAGGAAGCTCTATCTATCTTCTTAATATCTTAATAATTTTATA 1495

QY 1962 CAGAAAATCTT-----TCAATATGCTGCTACCTAAATGATTTTGTGTTA 2011

Db 1494 GAGCTTTATTTCTCTAGACTATTTTATAGTTTCTTAAGTAATTTATTTCTTAGCTT 1435

QY 2012 CTAAATAATCTTTACCACTTAAAGCAAGCTAACATCTCTTAAGCTGATCAGGGA 2071

Db 1434 AGTTATTAATTAATAATTAATTAATAAGTTTAGTAACAGTTTCAAGGTTCAACTATAT 1375

QY 2072 TTTTGTGATATAAGCTGTTGTTAA-TCTGTATTAATTCAGTCGATTTTCAGTTCTGATA 2130

Db 1374 TTATATATTTTAAATTAATTAATTAATTTCTTTAGTATTACTAAGATTTAAGTTTACTTA 1315

QY 2131 TGTTAAGTAATCACTATATGAAGAAATTTGCTGTATAGCATCATTTATTTTACG 2190

Db 1314 GATTAATATCTATTTTATATATATATTCAGTTTATAGTACTATTTTATATATTTAAGT 1255

QY 2191 CTTTCTGTATAAAGCTTTTACTATTTCTGCTCGGCTTATTTATACATATATCTTT 2250

Db 1254 TAATTAATTTCTACCTGCTAGTATATCTTATTTATAGTATATAATAATATATCTAGGCA 1195

QY 2251 AATTAAATCTTTAACCACTAAATTTTCAAAATACCAGTGTGATATACATAGGAATCATTTAT 2310

Db 1194 AGCTGCTAGCTTACCTAGTATATTTTAAATTAATAAATAAATAATTAAGTATATCTGTC 1135

QY 2311 CAGAACTAGTCTGGTCTTTAGGAAGTATTAAAT-----AAGAAAATTTGCACATAACTT 2364

Db 1134 TAATATATTTACTATTATTATAAATATCTAATTTATAGTAAAGTATAGTAGTTTATATA 1075

QY 2365 AGTTGATTCAGAAAGGACTTGTAAGTGTGTTTTCTCCCAAAAGAGACTCTTTTTCACAC 2424

Db 1074 TTTATAATAATAATAAATTTTAAACTTTATAAGCTCTAATTTCTAAACTTTTAAAGCTA 1015

QY 2425 TAAACACTTTTTTAAAGGCTTATCTTGGCTCTCCCAACA-----AGAAGCAATAG 2476

Db 1014 TTAATAATTTACTAATAATTTTATTAATAAATTTTATAATTAATTTTGCAGGAGAGTTTC 955

QY 2477 TCTCCAGTCAATATAAATTTCTACAGAAATAGTGTCTTTTCTCCAGAAAAGCTTG 2536

Db 954 TTAATAATAATAATAAATAATAGTACTTTATTTATTTATATATATAATAATATTTTTC 895

QY 2537 TGAGATCATTAATAACATGTGACAAATTTAGAGATTTCTTTGTTTTTATTTTCTCATTATA 2596

Db 894 TAGTAGTCTAGTTTAATAATAAGAGCTTTAAATAATTTCTTAAATTTAGGATTAATAATA 835

QY 2597 TACTGTGGCAATTAACAGATTTATAAATTTTTTACAAAGCTATAGTATATATTTATTTG 2656

Db 834 TAAATAAGAGTTATATAAATAATTTATTTAGTATTATAACTAGGTATATCTTCTTAA 775

QY 2657 AATGGGAAAAGTGCAATTTTACTGTATTTTGTGTTATTTTCTCAGAAATAGGA 2716

Db 774 TCTATAAAAATTTAATAAATTTTATATTAAGATAGTAAAGTAGGTATATCAGGCTTAAGA 715

QY 2717 AAGAAATTAATGCTCAATAAATAT 2744

Db 714 AGTTTATATAAATAATTAATAAATTTAT 687

RESULT 7

US-10-204-708-86

; Sequence 86, Application US/10204708

; Patent No. 6677731

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

; APPLICANT: PIEPENBROCK, Christian

; APPLICANT: BERLIN, Kurt

; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

; FILE REFERENCE: 5013-1012

; CURRENT APPLICATION NUMBER: US/10/204,708

; CURRENT FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: PCT/EP01/03971

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: DE 10019058.8

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: DE 10043826.1

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 98

; SEQ ID NO 86

; LENGTH: 11050

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-86

Query Match

Best Local Similarity 53.0%; Pred. No. 0.007;

Matches 106; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 2568 GATCTTTGTTTATTTCTACTGATTAATATCTGTGGCAAAATTACACAGATTATAAATT 2627

Db 4259 GTTGGTTTCTTTTATTTTAAAGTATTTTATTTGTTAAATTTAATTTAATAG 4318

QY 2628 TTTTACAGAGTAGTAGTATATTTTGAAGTGGAAAGTGCATTTTACTGTATTTTG 2687
 Db 4319 TTTTTCGGTTTTTCGATAATTTTTTTGAAGTGTAAAGTAAATATTTTATTTAGTTTT 4378
 QY 2688 TGTATTTTCTTTTCTCAGAAATATGGAAGAAATTTAAATGTGTCAATAAATATTTT 2747
 Db 4379 TTATTTAGTTTGTAGTTATTTATAAAGAAATATTCTAAGGTTTAGTTAAATTTT 4438
 QY 2748 CTAGAGAGTAAAAAATAA 2767
 Db 4439 TTTAATATTTATGTAAAAA 4458

RESULT 8

US-08-998-416-683
 ; Sequence 683, Application US/08998416
 ; Patent No. 6239264
 ; GENERAL INFORMATION:
 ; APPLICANT: Philippsen, Peter
 ; APPLICANT: Pohlmann, Rainer
 ; APPLICANT: Steiner, Sabine
 ; APPLICANT: Mohr, Christine
 ; APPLICANT: Wendland, Jurgen
 ; APPLICANT: Knechtie, Philipp
 ; APPLICANT: Rebeschung, Corinne
 ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1152
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6239264artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: No. 6239264th Carolina
 ; COUNTRY: USA
 ; ZIP: 27709

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/998,416
 ; FILING DATE: 24-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: CH 0016/97
 ; FILING DATE: 31-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8587
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 683:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 724 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: FAG1453RP
 ; US-08-998-416-683

Query Match 1.8%; Score 49; DB 3; Length 724;
 Best Local Similarity 46.6%; Pred. No. 0.0015;
 Matches 267; Conservative 0; Mismatches 295; Indels 11; Gaps 3;
 QY 2199 TTAATAAGCTTTACTATTCTGTCCCTGGGCTTATATACATATTAAGTGTATTAAT 2258
 Db 149 TAAAGAAATGAATATTGTGGCACTCTTAATTTTATTTATTTAATGATTATTAATCT 208

QY 2259 ACTTAACCACTAATTTTGAAGATTTACCAGTGTGATACATAGGATCATTATTACAGATGT 2318
 Db 209 ATTTAAACATAAAACATTTTAAATGTTTATAAATAAATAAAGAAATTAATCTTAT----AGAA 264
 QY 2319 AGCTGCTCTTTAGGAAGTATTTAATAAGAAATTTGCACATAACTTAGTTGATTCAGAAA 2378
 Db 265 TATTTATTAATAGTATTTAATTTAATTTTAAATTAATTAATATACCATTTTATTAATAA 324
 QY 2379 GGACTTGTATGCTGTTTTTCTCCCAATGAAGACTCTTTTGGACACTAAACACTTTTTAA 2438
 Db 325 TAGATTATTAAAGTTTATTAATATTAAAGTGATATATAATTTAATTTATATAAATTTTAA 384
 QY 2439 AAAGCTTATCTTGCCTTCTCCAAACAAGAAAGCAATAGTCTCCCAAGTCAATATAAATCT 2498
 Db 385 TTACTTTCATGTATATATAATTTAATTAATGTACCTTTCATAATATTATTTTATTAG 444
 QY 2499 ACAGAAATAGTGTCTTT-----TTCACAGAAATGCTGTGAGAAATCAITTAACA 2553
 Db 445 TCTAGTAATATTTCTATTTAATAGTCTACCCCTTTAATTTGGATATTACTACTACTAATA 504
 QY 2554 TGTCACAATTTAGAGATTTCTTTGTTTATTTCACGTAAATTAATATACCTGTGCAATTTACA 2613
 Db 505 TTACCTTAATAATATATTATTAGAATCTTAATCTAATAATTTATTTCTAAGTATA 564
 QY 2614 CAGATTATTAATTTTACAGAGTATAGTATATTATTGAAATGGGAAAGTGCAT 2673
 Db 565 TAAATTAATTAATCTTTTATTATTAT--TTAAATTTATTAAATAGTAAATTTATAT 622
 QY 2674 TTTACTGTATTTGTGTATTTTGTATTCTCAGAAATATGGAAGAAATTTAAATGTTG 2733
 Db 623 TTATTATTTTAAACATAATTTTTTTGATAATATATATCATTAATTAATGTTAATTTA 682
 QY 2734 TCAATAAATATTTCTAGAGAGTAAAAAATAA 2766
 Db 683 TTAATAATTATCTTTTAATGAATTTAATGATAA 715

RESULT 9

US-08-446-855A-1/c
 ; Sequence 1, Application US/08446855A
 ; Patent No. 5849573
 ; GENERAL INFORMATION:
 ; APPLICANT: Stewart, Thomas S
 ; APPLICANT: Flores, Maria V
 ; APPLICANT: O'Sullivan, William J
 ; TITLE OF INVENTION: Nucleotide sequence encoding carbanoyl
 ; TITLE OF INVENTION: phosphate synthetase II
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon & Vanderhye PC
 ; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,855A
 ; FILING DATE: 06-Jul-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mitchard, Leonard C
 ; REGISTRATION NUMBER: 29,009
 ; REFERENCE/DOCKET NUMBER: 47-80
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-446-855A-1

Query Match
Best Local Similarity 47.3%; Score 49; DB 2; Length 8920;
Matches 148; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 2456 TCTCCAAACAAGCAATAGTCTCCAAAGTCAATATAAATCTACAGAAATAGTGTCT 2515
DB 8920 TCTAGAATAAGGAAAAAACAATATATATATATATATATATATATATATATATAGTCCC 8861
QY 2516 TTTTCTCCAGAAAAATGCTTGTGAGAAATCAATTAACATGTGACAAATTTAGAGATCTCTT 2575
DB 8860 TTTTGATATACAGTTCCTCTTTTTCGTTGAATTTTTTAAAAAATCATACATTTA 8801
QY 2576 GTTTTATTTCACTGATTAATATACGTGCGCAAAATACAGATTAATAAATTTTTTACA 2635
DB 8800 TAAATTTATATATAATTAAGAAATTTATACATTTTAATGTTTATATATATTTT 8741
QY 2636 AGAGTATAGTATATTTATTTGAAATGGGAAAGTGCATTTTACTGTATTTTGTGATTTT 2695
DB 8740 TTATAATTAATAAATTTATTAATAATTTATAAAATTTATTTGTAATGAAAAACCATTTTG 8681
QY 2696 GTTTTATTTCTCAGAAATATGAAAGAAATTAATAATGTGCAATATAATTTTCTAGAGAG 2755
DB 8680 GTTTATACATATGAGTGAATAATAAATTTGTATATATAACAAAAATTTATAAAAAAT 8621
QY 2756 TAAAAAATAAAA 2768
DB 8620 AAATCAATATAA 8608

RESULT 11
US-08-920-812-6/c
; Sequence 6, Application US/08920812
; Patent No. 5763188
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsunisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 8300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,812
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-22
; US-08-920-812-6

Query Match
Best Local Similarity 47.4%; Score 48.8; DB 1; Length 8654;
Matches 175; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-09-150-741-1/c

Query Match
Best Local Similarity 47.3%; Score 49; DB 3; Length 8920;
Matches 148; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 2456 TCTCCAAACAAGCAATAGTCTCCAAAGTCAATATAAATCTACAGAAATAGTGTCT 2515
DB 8920 TCTAGAATAAGGAAAAAACAATATATATATATATATATATATATATATATATAGTCCC 8861
QY 2516 TTTTCTCCAGAAAAATGCTTGTGAGAAATCAATTAACATGTGACAAATTTAGAGATCTCTT 2575
DB 8860 TTTTGATATACAGTTCCTCTTTTTCGTTGAATTTTTTAAAAAATCATACATTTA 8801
QY 2576 GTTTTATTTCACTGATTAATATACGTGCGCAAAATACAGATTAATAAATTTTTTACA 2635
DB 8800 TAAATTTATATATAATTAAGAAATTTATACATTTTAATGTTTATATATATTTT 8741
QY 2636 AGAGTATAGTATATTTATTTGAAATGGGAAAGTGCATTTTACTGTATTTTGTGATTTT 2695
DB 8740 TTATAATTAATAAATTTATTAATAATTTATAAAATTTATTTGTAATGAAAAACCATTTTG 8681
QY 2696 GTTTTATTTCTCAGAAATATGAAAGAAATTAATAATGTGCAATATAATTTTCTAGAGAG 2755
DB 8680 GTTTATACATATGAGTGAATAATAAATTTGTATATATAACAAAAATTTATAAAAAAT 8621
QY 2756 TAAAAAATAAAA 2768
DB 8620 AAATCAATATAA 8608

RESULT 10
US-09-150-741-1/c
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1

Query Match
Best Local Similarity 47.3%; Score 49; DB 3; Length 8920;
Matches 148; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 2456 TCTCCAAACAAGCAATAGTCTCCAAAGTCAATATAAATCTACAGAAATAGTGTCT 2515
DB 8920 TCTAGAATAAGGAAAAAACAATATATATATATATATATATATATATATATATAGTCCC 8861
QY 2516 TTTTCTCCAGAAAAATGCTTGTGAGAAATCAATTAACATGTGACAAATTTAGAGATCTCTT 2575
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2391	QY	TGTTTTCTCCAAATGAGAGCTCTTTTTTGACACTAAACACACTTTTTTAAAAGCTTATCTT	2450
2499	Db	TGTTTTAAATCTACAAAAGAGAGAAGTAACATACAAAAGAGTTTAAAAGTGCGGTATATT	2540
2451	QY	TGCGTTCTCCAAACAGAACCAATAGTCCTCCAAAGTCAATATAAATCTCTAC - AGAAAAATA	2508
2439	Db	AATATAACTTAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTCTCTCTAAATTTA	2380
2509	QY	GTGTTCTTTTTCTCCAGAAAAAATGCTTTGTGAGAAATCATTTAAAAACATGTGACAAATTTAGAG	2568
2379	Db	ATAAAAATTTATATATATAAAAAATGTTAGTAAAAATCTTCCAAAAAGTATCTCTTTTAGT	2320
2569	QY	ATCTTTGTTTTTAATTTCACTGATTAATATACTGTGGCAAAATTCACAGATATATAAATTT	2628
2319	Db	ATAAATTTTTTAAATTAAGGAAAAATTAGAAAAAATCTTATTTTTTTTGAATATAGCAAAAT	2260
2629	QY	TTTTTACAAGATATAGTATATATTTTATTTGAATGGGAAAGTGCAATTTTACTGTATTTGT	2688
2259	Db	GCTACATTCGTAATTCAGGTATATAACTTTTAAAAAGATAATTTGTGTTTATAAACACTTATTT	2200
2689	QY	GTATTTTGTTTTATTTCTCAGATATATGAAAGAAAAATTAAAAATGTGCAATAAAAATTTTC	2748
2199	Db	GTTTACTCTCTTAATTTTATTTAGTTTATTAATTAATCTAAATTAATATAGCAATTAATATATTC	2140
2749	QY	TAGAGAGTAAAAAATAA	2766
2139	Db	TTTAAATTTTAAATTAATA	2122

RESULT 12

US-08-920-827-6/C
Sequence 6, Application US/08920827
Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotosugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8654 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

	Molecule Type:	Genomic DNA	
	Original Source:		
	Organism:	Staphylococcus epidermidis	
	Strain:	Clinical Isolate SE-22	
	US-08-920-827-6		
	Query Match	1.8%; Score 48.8; DB 1; Length 8654;	
	Best Local Similarity	47.4%; Pred. No. 0.0099;	
	Matches 179; Conservative	0; Mismatches 197; Indels 2; Gaps 1;	
QY	2391	TGTTTTCTCCAAATGAAGACTCTTTTGGACATAAACACATTTTAAAAAGCTTATCTT	2450
Db	2499	TGTTTTAATTCTACAAAAGAGAAGTAACATCAAAAAGAGTTTAAAAAGTGCGGTATATT	2440
QY	2451	TGCCCTTCCTCAAACAAGAGCAATAGTCTCCAAGTCAATATATAAATCTCTAC--AGAAAAATA	2508
Db	2439	AATATAACTAAGGCCTTATTGATAGTAGAAAAGTGTGTAAAAACCTTACTCTAATTA	2380
QY	2509	GTGTTCTTTTTCTCCAGAAAAATGCTTTGGAGAAATCATTTAAACATGTGCAGAAATTTAGAG	2568
Db	2379	ATPAAACATTTATATATAAAAAATGTTAGTAAAAATTCCTTCCAAAAGTAGTCTCTTTTAGT	2320
QY	2569	ATTCCTTTGTTTTATTTTCACTGATTAATATATACGTGCAAAATACACAGAAATTTAAATTT	2628
Db	2319	ATAATTTTTTATTAATANGAANAATTAGAACAATCTTATTTTTTGAATATAGCAAT	2260
QY	2629	TTTTACAAGAGTATAGTATATTTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT	2688
Db	2259	GCTACATTCCTAATTCAGATAAATCTTTTAAAAGATAATTTGTTTTTATAACACATTTATT	2200
QY	2689	GTATTTTGGTTATTTCTCAGATATGGAAGAAAAATTTAAAAATGTGTGCAATTAATATTTTC	2748
Db	2199	GTTTACTCTCTAATTTTTTATTTAGTTATAATTAACATAATATATAGCATTAATATATTC	2140
QY	2749	TAGAGAGTAAAAAAAAA	2766
Db	2139	TTTAAATTTTAAATTAATA	2122

RESULT 13

US-08-921-177-6/C
Sequence 6, Application US/08921177
Patent No. 5798211
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-taures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 190366/32420

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8654 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Staphylococcus epidermidis
 STRAIN: Clinical isolate SE-22
 US-08-921-177-6

Query Match 1.8%; Score 48.8; DB 1; Length 8654;

Best Local Similarity 47.4%; Pred. No. 0.0099;
 Matches 179; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

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QY 2391 TGTCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2450
DB 2499 TGTCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2440
QY 2451 TGCCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2508
DB 2439 AATATACTAAAGCTTATTGATAGATGAAGAGTTTAAAGCTTCTTCTTAAATTA 2380
QY 2509 GTGCTCTTTTCCAGAAAATGCTTGTGAGAAATCAATTAACATGACAAATTTAGAG 2568
DB 2379 ATAACATTTATATATAAAAGATTTAGTAAATCTTTTCCAAAAGATTTCTTTTAGT 2320
QY 2569 ATTCTTTGTTTATTTCACTGATTATATATACGTGCGCAATTTTACACAGATTATTAATTT 2628
DB 2319 ATAATTTTATTAATTAAGGAAATTAAGAAATCTTATTTTTCGAATATAGCAAT 2260
QY 2629 TTTTACAAGATAGTATATTTATTTGAAATGGGAAAAGTCATTTTACTGTTATTTGT 2688
DB 2259 GCTACATTGCTAATCAAGTATAAACTTTTAAAGATAATTTGTTTATAACACATTTAT 2200
QY 2749 TAGAGAGTAAAAAATA 2766
DB 2139 TTTAATTTAATTAATA 2122

```

RESULT 14

US-08-362-577C-6/c

Sequence 6, Application US/08362577C
 Patent No. 5807673

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
 APPLICANT: Matsuhisa, Akio
 APPLICANT: Uehara, Hirotsugu
 APPLICANT: Eda, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,577C
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Rin-Laures, Li-Hsien
 REGISTRATION NUMBER: 33,547
 REFERENCE/DOCKET NUMBER: 19036/32420
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8654 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Staphylococcus epidermidis
 STRAIN: Clinical isolate SE-22
 US-08-362-577C-6

Query Match 1.8%; Score 48.8; DB 1; Length 8654;

Best Local Similarity 47.4%; Pred. No. 0.0099;
 Matches 179; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

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QY 2391 TGTCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2450
DB 2499 TGTCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2440
QY 2451 TGCCTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTAAAGCTTATCTT 2508
DB 2439 AATATACTAAAGCTTATTGATAGATGAAGAGTTTAAAGCTTCTTCTTAAATTA 2380
QY 2509 GTGCTCTTTTCCAGAAAATGCTTGTGAGAAATCAATTAACATGACAAATTTAGAG 2568
DB 2379 ATAACATTTATATATAAAAGATTTAGTAAATCTTTTCCAAAAGATTTCTTTTAGT 2320
QY 2569 ATTCTTTGTTTATTTCACTGATTATATATACGTGCGCAATTTTACACAGATTATTAATTT 2628
DB 2319 ATAATTTTATTAATTAAGGAAATTAAGAAATCTTATTTTTCGAATATAGCAAT 2260
QY 2629 TTTTACAAGATAGTATATTTATTTGAAATGGGAAAAGTCATTTTACTGTTATTTGT 2688
DB 2259 GCTACATTGCTAATCAAGTATAAACTTTTAAAGATAATTTGTTTATAACACATTTAT 2200
QY 2689 GTATTTGTTTATTTCTCAGATATGGAAGAAAATTAAGTGTCTCAATTAATTTTC 2748
DB 2199 GTTACTTCTTAAATTTTATTTAGTTAATAATTAATAATATAGCATTAATATTC 2140
QY 2749 TAGAGAGTAAAAAATA 2766
DB 2139 TTTAATTTAATTAATA 2122

```

RESULT 15

US-08-320-828-6/c

Sequence 6, Application US/08920828

Patent No. 5853998

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
 APPLICANT: Matsuhisa, Akio
 APPLICANT: Uehara, Hirotsugu
 APPLICANT: Eda, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America

ZIP: 60506-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8654 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical isolate SE-22
US-08-920-828-6

Query Match 1.8%; Score 48.8; DB 2; Length 8654;
Best Local Similarity 47.4%; Pred. No. 0.0099;
Matches 179; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

QY	2391	TGTTTTTCTCCCAATGACGACTCTTTTGACACTAAACACCTTTTAAAGGCTTATCTT	2450
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QY	2689	GTATTTTGTATTCTTCAGAAATGGAAGAAAAATTAATGTCGAATAATATTTTC	2748
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QY	2749	TAGAGCTAAAAAATAA 2766	
Db	2139	TTTAAATTTAAATTAATA 2122	

Search completed: May 17, 2004, 08:41:27
Job time : 194.781 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: May 17, 2004, 07:43:11 ; Search time 10751.2 Seconds
(without alignments)
11159.041 Million cell updates/sec
Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tgcagccaccattttaag.....tagagagtaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	2393.8	86.5	2397	9	AX358703	AX358703 Homo sapi
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9	1538	55.6	158789	2	AC146259	AC146259 Pan trogl
10	863.4	31.2	96782	9	AL592436	AL592436 Human DNA
11	861.8	31.1	208942	2	AP001393	AP001393 Homo sapi
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13	596.4	21.5	251308	2	AC023234	AC023234 Mus muscu
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15	572.2	20.7	221680	2	AC116288	AC116288 Rattus no
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17	390.8	14.1	1683	5	BC054563	BC054563 Danio rer
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19	383	13.8	383	6	AX334593	AX334593 Sequence
20	323.4	11.7	425	6	AX193026	AX193026 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS BC031265 2577 bp mRNA linear PRI 07-OCT-2003
DEFINITION Homo sapiens transmembrane 4 superfamily member 12, mRNA (CDNA
clone MGC:39733 IMAGE:5275953), complete cds.
ACCESSION BC031265
VERSION BC031265.1 GI:21411498
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2577)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, E., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, J., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellon, B., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16893-16903 (2002)

22388257

12477932

2 (bases 1 to 2577)

Strausberg, R.

Direct Submission

Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-rc@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mdc@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 63 Row: j Column: 1.

Location/Qualifiers

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433. .1116

/note="transmembrane4; Region: Tetraspanin family"

misc_feature

source

FEATURES

db_xref="CDD:pfam00335"

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;

Matches 2566; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 195 GGCCTGGCTGCGCGCGCTGCTCCGACCTCCGAGAGGACTTCGGAGGACACGCGC 254

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QY 255 GCTGGAGAGTGGCTTAGCAGAGACTTTCACGCAACTGCTGCCAGAGACTTTTTTTTT 314

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QY 315 TTTTCTTTTCCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 374

DB 119 TTTTCTTTTCCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 178

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RESULT 2

AX092376

LOCUS 2397 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 107 from Patent WO0116318.

ACCESSION AX092376

VERSION AX092376.1 GI:13444502

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eaton,D.L., Pilvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0116318-A 107 08-MAR-2001; Genentech, Inc. (US)

FEATURES

source

1. .2397

/organism="Homo sapiens"

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ORIGIN

Query Match 86.5%; Score 2393.8; DB 6; Length 2397;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 LOCUS
 DEFINITION
 Sequence 323 from Patent WO0168848.
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 AX376256
 VERSION
 AX376256.1 GI:19170519
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 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
 Zhang, Z.
 TITLE
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL
 Patent: WO 0168848-A 323 20-SEP-2001;
 Genentech, Inc. (US)
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LOCUS Homo sapiens clone DNA6880 NET-2 (UNQ774) mRNA, complete cds.

DEFINITION AY358703
ACCESSION AY358703.1 GI:37182527
VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2397)
AUTHORS

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wiesand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,W., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309
2 (bases 1 to 2397)
Clark,H.F.

Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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FEATURES
source

gene

CDS

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ORIGIN

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DB	1261	TGCTTTAAATGAGGATGGAAGATTTTCAATGCTAATGTCACCACTGGACATATTTGA	1320		
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DB	1321	TGCCCTTAAATGCTGAAGACAGATGTCATCCACTGTGTAGCTGTGTATGACCTTTTA	1380		
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DB	1441	CGAGTCATATGCTGGGACTGGAGCCATAGTAAGTGTGATTTACTTCTACCACTAGT	1500		
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DB	1801	TTGTCTCTGTATAGCATCATTTATTTTAGCTTTTCTGTTTAAAGCTTTACTTTCTGT	1860		
QY	2222	CCTGGGCTTATATACACATATACCTGTTTAAATATCTTACCACTAATTTTGAAT	2281		
DB	1861	CCTGGGCTTATATACACATATACCTGTTTAAATATCTTACCACTAATTTTGAAT	1920		
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LOCUS Homo sapiens tetraspan NET-2 mRNA, complete cds.
DEFINITION
ACCESSION AF124522
VERSION AF124522.1 GI:4325291
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2267)
AUTHORS Serru, V., Dessen, P., Boucheix, C. and Rubinstein, E.
TITLE Sequence and expression of seven new tetraspans
JOURNAL Biochim. Biophys. Acta 1478 (1), 159-163 (2000)
MEDLINE 20185353
PUBMED 10719184
REFERENCE 2 (bases 1 to 2267)
AUTHORS Rubinstein, E., Serru, V., Dessen, P. and Boucheix, C.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) INSERM U268, 14 Av Paul Vaillant Couturier,
Villejuif 94807, France
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ELLKPSLSRIFETSINANSFNTHFEMEEL"

ORIGIN

Query Match 81.7%; Score 2260.2; DB 9; Length 2267;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2262; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 61 TCACAATGGCCAGAGAGATTCGGTGAAGTGTCTGCGTGCCTGCTCTACGCCCTCAATC 120
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Db 121 TGCTCTTTTGGTAAATGTCCATCAAGTGTGTGGCAGTTCCTGCTTGGATGAGGACTACC 180
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Db	1201	GATGTCATACCCACTGCTGTAGCTGTGTATGACTTTTACTGAACACAGTATGTTTTCAG	1260
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Db	1261	GCAGCATGTTTGAATAGCATTTCCGCATCCATGCAAGAGTCAATATGGTGGGACGTG	1320
QY	1824	GAGCCATAGTAAAGGTTGATTTACTTCTACCACTAGTATATAAAGTACTAATTAATGTC	1883
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Db	1381	TAACTAGGAAGTTAGAAAATCTAATAACTTTTATTTACTGAGCATCTATTTCTCTGAT	1440
QY	1944	GCTTAATAATATATATATCAGAAAATCTTTCAATATTTGGTACTACCTAAATGTGATTTT	2003
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DEFINITION	BD269117		
ACCESSION	BD269117.1	GI:33078885	
VERSION	JP 2002543848-A/8.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	1 (bases 1 to 1807)		
AUTHORS	Ruben, S.M., Ni, J., Fan, P., Roschke, V., Shi, Y., Komatsoulis, G.A. and		
TITLE	Rosen, C.A.		
JOURNAL	Patent: JP 2002543848-A 8 24-DEC-2002;		
COMMENT	HUMAN GENOME SCIENCES INC		
	OS Homo sapiens (human)		
	PN JP 2002543848-A/8		
	PD 24-DEC-2002		
	PF 18-MAY-2000 JP 2000618481		
	PR 19-MAY-1999 US 60/135122, 03-JUN-1999 US 60/137797 PR		
	11-JUN-1999 US 60/138573, 18-AUG-1999 US 60/149447 PR		
	28-JAN-2000 US 60/178770		
	PI STEVEN M RUBEN, JIAN NI, PING FAN, VIKTOR ROSCHKE, YANGGU SHI, PI		
	GEORGE A KOMATSOLIS, CRAIG A ROSEN		
	PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P7/02,		
	PC A61P9/10,		
	PC A61P25/14, A61P25/16, A61P25/18, A61P25/28, A61P35/00, C07K14/705,		
	PC C07K16/28,		
	PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, G01N33/15, G01N33/ PC		
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RESULT 8

AC004456/c

LOCUS

DEFINITION

AC004456

AC004456.1

VERSION

HTG

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 143436)

Sulston, J.E. and Wilson, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

PUBMED

9847074

2 (bases 1 to 143436)

Antonou, B. and Le, F.

The sequence of Homo sapiens PAC clone RP5-1100F23

Unpublished (2001)

3 (bases 1 to 143436)

Waterston, R.

Direct Submission

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4 (bases 1 to 143436)

Waterston, R.

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Submitted (03-FEB-2000)

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5 (bases 1 to 143436)

Wilson, R.

Direct Submission

Submitted (15-OCT-2003)

Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>Contact: sapiens@wustl.edu

----- Summary Statistics

Center project name: H_DJ1100F23

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at <http://www.chori.org> using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc.

(<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP5-872F7. Actual start of this clone is at base position 1 of RP5-1100F23 actual end is at 143436 of RP5-1100F23. The orientation of this clone is unknown.

FEATURES

source

Location/Qualifiers

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Best Local Similarity 98.8%; Pred. No. 0; Mismatches 23; Indels 0; Gaps 0;
Matches 1596; Conservative 0;

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RESULT 9
ACL46259/c

LOCUS Pan troglodytes chromosome UNK clone R943-28H17, *** SEQUENCING IN
DEFINITION AC146259 .158789 bp DNA linear HTG 01-AUG-2003
PROGRESS ***, 8 unordered pieces.

ACCESSION AC146259

VERSION AC146259.1 GI:33387212

KEYWORDS HTG; HTGS PHASE1

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 158789)
AUTHORS Wilson, R.K.
TITLE The sequence of Pan troglodytes clone

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158789)
AUTHORS Wilson, R.K.

DIRECT SUBMISSION

TITLE Submitted (01-AUG-2003)

JOURNAL Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: C_PT028H17

----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-terminator ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 155793 bases at least Q40
 Consensus quality: 156306 bases at least Q30
 Consensus quality: 156616 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 5105: contig of 5105 bp in length
 * 5106: gap of unknown length
 * 5206: contig of 3740 bp in length
 * 8945: gap of unknown length
 * 9046: contig of 7877 bp in length
 * 16922: contig of 14067 bp in length
 * 31089: contig of 14067 bp in length
 * 31090: gap of unknown length
 * 31190: contig of 2227 bp in length
 * 53417: gap of unknown length
 * 53517: contig of 50650 bp in length
 * 104166: gap of unknown length
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FEATURES

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RESULT 10
AL592436/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCES
AUTHORS
TITLE
JOURNAL
COMMENT

AL592436 Human DNA sequence from clone Rp11-710N8 on chromosome 1, complete sequence.
AL592436 AL592436.7 GI:16973137
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96782)
Ramsay, H.
Direct Submission
Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:16151298.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assemblies were confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

RP11-710N8 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-710N8. It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-710N8 is at 1 in this sequence. The true left end of clone RPS-929G5 is at 94783 in this sequence.

FEATURES
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ORIGIN
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Best Local Similarity 79.5%; Pred. No. 1.4e-171;
Matches 1236; Conservative 0; Mismatches 266; Indels 53; Gaps 16;
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Db 35483 ACATACATCTTTGCAACACACTTTTATACACCTTTTGAATGAGTAAATATTA- -G 35427
QY 1492 AATGTCAAGAGAAACCAAACTTGTGTTTCTGAGCTTGTGAATTTTGTAGTACATA 1551
Db 35426 AATGTCAAGAGAAACCAAACTTGTGTTTCTGAGCTTGTGAATTTTGTAGTACATA 35367
QY 1552 C-TATGTGTTTTCAGAAATATGAGAAATGTTGCCATAAATAAATCAACCTTAAGCAT 1610
Db 35366 CTTAACTGTTACAGAAATTTGAGAAATTAACATGTTGCTATAAGAAATGCTCTGGGAT 35307
QY 1611 ATACTATTCTATGCTTTTAAATGAGGATGGAAGTTTCAATGATAGTCAACCTGG 1670

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* 125416 137713: contig of 12298 bp in length
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* 147895 147994: gap of 100 bp
* 147995 156594: contig of 8600 bp in length
* 156595 165511: contig of 8817 bp in length
* 165512 165611: gap of 100 bp
* 165612 172481: contig of 6869 bp in length
* 172481 172580: gap of 100 bp
* 172580 182109: contig of 9529 bp in length
* 182109 182209: gap of 100 bp
* 182210 187931: contig of 5722 bp in length
* 187931 188031: gap of 100 bp
* 188031 193656: contig of 5625 bp in length
* 193656 193757: gap of 100 bp
* 193757 199153: contig of 5397 bp in length
* 199154 199253: gap of 100 bp
* 199254 203762: contig of 4509 bp in length
* 203763 203862: gap of 100 bp
* 203863 207517: contig of 3655 bp in length
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* 207618 208942: contig of 1325 bp in length.

FEATURES

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QY 952 GGTCACTTTGAAAGCCAGGATGACAAATATGGATTACCTAGATATCGTGGCTTACTCA 1011
Db 58391 AGTCACCTTTGAAAGCCAGGATGAGCAAA-TATGACTTACCTGATGACCAAGTGGCTTACTCA 58323
QY 1012 TCGTTGGAATTTTTTTCAGAGAGAGTTTAAGTGTCTGGAGTAGTATATTTTCACTGACTG 1071
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QY 1072 GTTGGAAATGACAGATGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAAATTCGCCAGG 1131
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Db 58163 CAAAA-ATGTTTTCCTTTTGAAGGAACCAACAACTGAGGTGCTGAGGTTCCTGGGAAT 58105
QY 1252 CTCATTGGGTGACACAAATCCTGGCATGATTCTCACCATTACTCTGCTCTGGGTCT 1311
Db 58104 TTCCATTAAAGTGACACAAA-CCTGGCCATGATTCTCACCATTACTTAACTCTGGGTCT 58046
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QY 1671 ACAATAATTGATG-CCCTTAAATGCTGAAGACAGATGTATACCCACTGTGTAGCTGT 1729
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Db 57519 CTACAGGTAGTATATAAAGTACCACACTGCTACATAGAAACAAACACAGTATAAA 57460
QY 1910 TAACTTTTACTCAGGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAAAC 1969

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QY      2257 ATACTTAACACTAATTTTGAATAATACAGTGTGATACATAGGAATCATTTATTCAGAT 2316
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LOCUS     Homo sapiens (human)
DEFINITION Homo sapiens
ACCESSION AX079479
VERSION   AX079479.1
KEYWORDS  Homo sapiens
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Baker, K.P., Goddard, A. and Wood, W.I.
TITLE     Human polypeptides and methods for the use thereof
JOURNAL   Patent: WO 01/0611-A 223 01-FEB-2001;
          Genentech, Inc. (US)
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QY      448 CGTCCCGGCTATCCCGACGCGGCGTGGGGCACCGGGCCGACGCGACGATCGCTGCC 507
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QY      508 GTTTGCCCTTGGAGTAGATGTGTGAAGAGTGGGGCTTCTCCCTTACGGGCTCAC 567

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QY      928 GGTTCCTCAGTACAATGTGATATGTGCTCACTTTTGAAGCCAGGATGACAAAATTATGAT 987
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DEFINITION DRAFT SEQUENCE, 46 unordered pieces.
ACCESSION AC023234
VERSION   AC023234.14
KEYWORDS  HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1
AUTHORS   Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R.,
          Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A.,
          Gordon, M., Goltz, J.S. and Kucherlapati, R.
TITLE     High Throughput Mouse Sequencing
JOURNAL   Unpublished
REFERENCE 2
AUTHORS   Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R.,
          Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A.,
          Gordon, M., Goltz, J.S. and Kucherlapati, R.
TITLE     Direct Submission
JOURNAL   Submitted (10-FEB-2000) Department of Molecular Genetics, Albert
          Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
          Bronx, NY 10461, USA
          On Aug 9, 2001 this sequence version replaced gi:14718674.
          -----Genome Center
          Center: Harvard Partners Genome Center
          Center Code: HPGC
          Web site: http://www.hpcg.org/Sequence/mouse.html
          Contact: hpgc@mdel.mgh.harvard.edu
          -----Summary Statistics
          Center project name: ABB
          Sequencing vector: pUC18; 108752
          Chemistry: Dye-terminator Big Dye; 100%
          *Consensus quality: 23188 at least Q20
          *Consensus quality: 225718 at least Q30

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*Consensus quality: 215659 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 250408 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 5.8 x in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 249287: contig of 1110 bp in length
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QY	1819	GACTGAGGCAATGAAAGGTTGATTTACTTCTACCACTAGTATATAAGTACTAATA	1878
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QY	1939	CTGATGCTAAATAAATATATATATCAGAAAACTTTCAATATTGTGTGACTACTACCTAAATGTGA	1998
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QY	2116	TTTCAGTTCTGATAATGTTAAGAAATAC--CATTTAGAAAGGAAATTTGTCCTGTATA	2173
Db	57855	TTTCAGTTCTGATAATGTTAAGAAATATTTGAAATGCGAAAAATTTGTCCTACACA	57914
QY	2174	GCATCATATTTTTCAGCTTTCTGTTTAAAGCTTTACTATTCTGTCTGGCTTATA	2233
Db	57915	GTACCATTTACTTTTGTCTCTTTTTCAG-CAACAGAACTTTTAAATCTCGTCTGTGTTCTGTA	57973
QY	2234	TTACACATATAAATCTGTT-ATTTAAATCTTAAACCACTAAATTTTGAAATTTACCACTGTGA	2292
Db	57974	CTATATCTATACTGTTAAATTTAAGTTGTTTAACTAACTAAATTTTGGAAATTTACCACTTTGA	58033
QY	2293	TACATGAGAAATCATTTATTCAGAAATGATCTGTGCTTTAGGAAGTATTATAAGAAATTT	2352
Db	58034	CACATAGGAATC-----TCTGTAACTGCTGCTGCGGAGAGTATTAACTACAGAAAT	58084
QY	2353	TGCACATAACTTATGATTTCAGAAAGGACTTGTATGCTGTTTCTTCCCAATTAAGAC	2412
Db	58085	TACACA-----TAGTTGATTCATCAAAAGTTCAAGTTTTCCTCCCTCCCAAAACACT	58139
QY	2413	TCCTTTTGACATPAAACACTTTTAAAGCTTATCTTTGCTCTTCCCTTCCCAACAGAGCA	2472
Db	58140	TTGTCAAGAGTGTCTTTTCGTTTTTATTTTAAATGTTTTCATGTTATTTCTTTTGCATCA	58199
QY	2473	ATAGTCTCCAGTCAATATAAATTTTACAGAAATAGTGTCTTTTCTCCAGAAAAATG	2532
Db	58200	AGAGCAACCACTTGAAGTTGATGTAATTTTACAGAGAAACCAATTTCTCTGAGAGATG	58259
QY	2533	CTTGTGAGAACTATAAACAATGTCACAAATTT-----AGAGATCTCTTTTATTATCA	2586
Db	58260	CTCATAGGAATCTTAAATTAAGTGTAGCTTAACCAAGAGAAATCTTGTATTTCTTCA	58319
QY	2587	CTGATTAATATCTGCGCAATTTACAGATTTATTAATTTTTCAGAGATATAGTA	2646
Db	58320	TCAATTAATACCTGTAGCAAAATGTCAGAAATTT-AAATTTTTCAGAGATAGAGA	58378
QY	2647	TATTTATTTGAAATGGGAAAGTCACTTTTACTGTATTTTGTATTTTGTATTCTCTC	2706
Db	58379	TATTTATTTGAAACGGGAAAGTGCATTTTACTGTATCTGTGCAATTTCTGTTCTTCTT	58438
QY	2707	AGATATGGAAGAAATTTAAATGTTCAATAAATTTTCTAGA	2752
Db	58439	GGATTCAGAGAAAGAAATTA-----TCAATAAATATTCTTCTAGA	58478
RESULT 14			
AC117109/c			
LOCUS	AC117109	188638 bp	DNA linear HTG 15-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-242N20, *** SEQUENCING IN PROGRESS		
	***, 7 unordered pieces.		
ACCESSION	AC117109		
VERSION	AC117109.4	GI:25013238	
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 188638)		

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, J., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerrero, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhera, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternack, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, R., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villasa, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

TITLE

Direct Submission
Unpublished
2 (bases 1 to 188638)

REFERENCE

Worley, K. C.

AUTHORS

Worley, K. C.

JOURNAL

Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

3 (bases 1 to 188638)

AUTHORS

Rat Genome Sequencing Consortium.

TITLE

Direct Submission

JOURNAL

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194558. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GTNB

Center Clone name: CH230-242N20
Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 171501 bases at least Q40
Consensus quality: 173679 bases at least Q30
Consensus quality: 175403 bases at least Q20
Estimated insert size: 173126; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 11978: contig of 11978 bp in length
* 11979 12078: gap of unknown length
* 12079 16868: contig of 4790 bp in length
* 16869 16968: gap of unknown length
* 16969 166286: contig of 149318 bp in length
* 166287 163386: gap of unknown length
* 163387 176280: contig of 9894 bp in length
* 176281 176380: gap of unknown length
* 176381 185754: contig of 9374 bp in length
* 185755 185854: gap of unknown length
* 185855 185977: contig of 1123 bp in length
* 185978 187077: gap of unknown length
* 187078 188638: contig of 1561 bp in length.

FEATURES

source

1. 188638
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-242N20"
complement(3794..4687)
/note="clone_boundary
clone_end:T7
site:
end_sequence:RXAAH82TJ"

misc_feature

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/note="wgs contig"

misc_feature

16969..18163
/note="wgs contig"

misc_feature

18299..18949
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misc_feature

complement(146665..147518)
/note="clone_boundary
clone_end:Sp6
site:
end_sequence:RXAAH82TV"

misc_feature

166387..168410
/note="wgs end extension
clone_end:Sp6"

ORIGIN

Query Match 20.7%; Score 572.2; DB 2; Length 188638;
Best Local Similarity 68.9%; Pred. No. 4.9e-110;
Matches 1107; Conservative 0; Mismatches 413; Indels 87; Gaps 20;

QY 1169 CTTTATCAAGAGGTTGTGGGAAGAAATGTATCTCTTTTGGAGGAGCAACCAACTG 1228
 Db 128329 CTTGTTTTACAGGTTGTGGGAAGAAATGTATCTCTTTTGGAGGAGCAACCAACTG 128270
 QY 1229 CAGGTCTGAGGTTCTGGGAATCTCCATTTGGGTGACACAAATCTGTCCTGATCTC 1288
 Db 128269 CAAGTACTAAGGTTCTGGGAATCTCCATTTGGGTGACACAAATCTGTCCTGATCTC 128210
 QY 1289 ACCATTACTCTGCTCTGGGCTCTGTATATATAGAGGAGCGCGGGACAGACCAAAATG 1348
 Db 128209 ACCATTACTCTGCTCTGGGCTCTGTATATATAGAGGAGCGCGGGACAGACCAAAATG 128150
 QY 1349 ATGTCCTTGAAGATGACAACTCTGAGCACTCTGATGTCCTCTGATGAGACTGTTGAAA 1408
 Db 128149 CTATCTCTAAATAATGATCGTCAACACACTTGTCTGTCACTCTGTGGAACTGTTAAA 128090
 QY 1409 CCAAGCCTGTCAAGATCTTTGAACACACATCCATGGCAACAGCTTTTAATACACACTT 1468
 Db 128089 CCAAGCCTTCTAGGATCTTTGAACACATCAATGCGCAACAGCTTCAATACCACTT 128030
 QY 1469 GAGATGGAGGAGTATPAAAAAGAAATGTCCAGAGAGAAAAACCAAACTTGTCTTCTGG 1528
 Db 128029 GAGATGGAGGAGTATPAAAAAGGATTAATTTATCCACTCTTTAAACAAAGCTTCCACAT 127861
 QY 1529 ACTTGTGAATTTTGTAGTACATCTATGTTTCAAGATATGTAGAAATGAATATGTTG 1588
 Db 127977 ACTAGTGGGTTTGGGGTACA---CAGCTATCTCAGAAATTTTATAGACATCTAATATC 127921
 QY 1589 CCATAAAATAACACCTPAAGCATATCTATTTCTATGCTTTAAATAGGAGTGGAAAGTT 1648
 Db 127920 TGAAGAGGAGTCTAAGCTTATAATTTATCCACTCTTTAAACAAAGCTTCCACAT 127861
 QY 1649 CATGTCATAGTCAACCTGGACATATTAATGATGCCCTTAAATGCTGAGACAGATGT 1708
 Db 127860 AAT-----ACACAGACAATACTAGCGTCTTTAAATGCTGGAACCCAGAGTT 127813
 QY 1709 CATACCCACTGTG-----TAGCCTGTGTATGACTTTTACTGAAACACAGTTATGTT 1758
 Db 127812 CATACCAACTGTGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTGACACAAATATGTT 127753
 QY 1759 TTGAGCAGACGTTGTTGATAGCATTCGGCATCCATGCAACCAAGCTCACAT---ATGG 1815
 Db 127752 TTGAGGTGATACAGTTTGTGACGCGTTTCTGCACTCCATTCATGGAATGAACGTGCATGG 127693
 QY 1816 TGGGACTGGAGCCATAGTAAGGTGATTTACTTCTACCACTAGTATATAAGTACTAA 1875
 Db 127692 GGGCACTCATGCTGTATGAAGTTAACTAATCTCT-CTAGTTAGCTATAAATCTTCA 127634
 QY 1876 TTAATTCCTAACATAGGAAGTTAGAAAATPACTAATACTTTTACTCAGCGATCTATT 1935
 Db 127633 CTGACTGCTAACATAGGATTTAG-----TGCTAAGACCTTTTATTACCTGATGATGTT 127578
 QY 1936 CTCTCATGCTAATAAATATATATACAGAAACCTTCATATTTGGTACTACCTAAATG 1995
 Db 127577 GCTTCAGCACTGATTTGATTAATAT-AAAAATCTTTCAAGGTGTTGTAAGTACTACCTAAATA 127519
 QY 1996 TGATTTTGTGTTGTTACTAAATATTTCTTACCACTTAAAGACGA---AGCTAACACATG 2053
 Db 127518 TGATTTTGTGTTGTTACTAAATATTTCTTATTAATGACACTTTGTAAGAGTAAACAGCTG 127459
 QY 2054 TCTTAAGCTGATCAGGAT-TTTTTGTATATAGTCTGTGTTAAATCTGTATAATCTAGT 2112
 Db 127458 TCTTAAACTTATCAGGATATATATGTTATAGTCTGTGCACTGCTGTATATAATCTAGT 127399
 QY 2113 CGATTTTCAGTCTGTAATGTTAAGATAACCAATAT---GAAAGAGGAAAATTTGCTCGT 2169
 Db 127398 AGATTTTCAGTCTTATTAATGTTACGAGACAATAATTTGAAATGACAAATTTGCTCTTA 127339
 QY 2170 TATGATCATATATTTTACGCTTCTCTGTTAATAAGCTTTTACTATTTCTGCTGGCT 2229
 Db 127338 TATAGCACCATTAATCTTTTCTCTCTCCCAACACAGAGCGTTTAAATGCGCTTGTGCTTC 127279
 QY 2230 TATATT-ACACATATACTGTT-ATTATAATCTTAAACCATAATTTTGAATAATTACCA 2287

Db 127278 TGATTTGTTACCCATCAGTGTAAATTTAAAGTTGTTAAACCAATTAATTTTGGAAATACCAG 127219
 QY 2288 TGTGATACATAGGAATCATATTAGAAATGAGTCTGCTCTTTAGGAAGTATTAAATAAGA 2347
 Db 127218 TGTGATACGTAGAAATCAT-----TGTAATCTGCTGCGAGGAGTATTAACTACA 127168
 QY 2348 AAATTGCAATAACTTGTGATTTAGAAAGGAGTCTGATGCTGTTTCTCCCAATG 2407
 Db 127167 GAATTTTACACA-----CAGTTGATTCAGCCAAAGTTTCACTGCTGCTTTTTCACCCAA 127113
 QY 2408 AAGACTCTTTTGACACTAAACACTTTTAAAGGCTTATCTTTGCTCTCTCCAAACAAG 2467
 Db 127112 TCTAGC-----CTGTCAAGAGCTTACGTTTCTTTTTCGACAAAG 127069
 QY 2468 AAGCAATAGTCTCAAGTCAATATAAATCTCAGAAATATAGTGTCTTTTCTCCAGAA 2527
 Db 127068 AAGCGACA-ACCTTGAAGTCAATGATTTTACAGAGGAGGAAATCTGTGAGAGATAA 127010
 QY 2528 AATGCTTGTGAGATCAATTAACATGTGACAAATTTAGAGATCTTTGTTTATTTCAC 2587
 Db 127009 TCATGGGAATCTCTAAATTAAGGGTATCTAATAGAGAGAGCTTGTCTTTATTC-- 126952
 QY 2588 TGATTAATATACCTGTGCGCAATTTACACAGATTTAAATTTTTCACAGATATAGTAT 2647
 Db 126951 --ATCCATATCTGTAGCAATTTATACAGATTTAAATTTTTCACAGAGTAGAAGAT 126894
 QY 2648 ATTTATTTGAAATGGGAAAGTCAATTTACTGATTTTGTGATTTTGTATTTCTCA 2707
 Db 126893 ATTTATTTGAAACGGGAAAGTCAATTTACTGATTTTGTGATTTTGTATTTCTTG 126834
 QY 2708 GAATATGGAAGAAATTA--AAATGCTCAATAAATATTTTCTTCTAGA 2752
 Db 126833 AATTAUGGAAGAAATTAATATACAGTGTCAATAAATATTTTCTAGA 126787

RESULT 15
 AC116288/c
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-400K6, *** SEQUENCING IN PROGRESS

 AC116288
 AC116288.4 GI:25138201
 HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
 Rattus norvegicus (Norway rat)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 221680)
 AUTHORS
 Muzny, D., Marie, M., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Altschuler, S., Amin, A., Anguiano, D.,
 Anvalbechi, V., Ayvagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gregoire, G., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M.,
 Hollins, B., Howell, S., Hui, S., Hume, J., Idlebird, D., Jackson, A.,
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

